Run on:

Title:

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; Search time 3180 Seconds (without alignments) 6998.376 Million cell updates/sec
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1 GAAGGGCAITGCTACAAGGI.....AITCTGCCTAGCCTGAAAAA 544
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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is the number of results predicted by chance to have a Pred. No.

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u	AK233033 Semience 1 from patent US 6489451.	AR259035	AR259035.1 GI:27309520		Unknown.	Unknown.	Unclassified.	1 (bases 1 to 544)	Li, B.X. and Cheng, X.	ntithrombosis enzyme fr	Patent: US 6489451-A 1 03-DEC-2002;	Location/Qualifiers
: 1 35	LOCUS A			KEYWORDS .	SOURCE	ORGANISM U	Þ	REFERENCE 1		TITLE A	ч	FEATURES

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421 CCAACCCTGCCTAGCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTCTCTGTA 480
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/organism="Deinagkistrodon acutus"
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98.0%; Pred. No. 1.3e-140;
iive 0; Mismatches 8;
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/clone="2100490"
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Cheng,X., Qian,Y., Liu,Q., Li,B.X.Y., Ding,J., Xu,Z., Huang,W. and
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Deinagkistrodon acutus
Beneragkistrodon acutus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu,H.-X., Xiang,K.-J. and Liu,J.
CDNA sequencing and analysis of eleven C-type lectin-like protein subunits from Agkistrodon acutus
Sheng wu hua hsueh, yu sheng wu wu li hsueh pao (2002) In press
                                                                                          1 GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGGCTTC
                                                                                                                 GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC
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Agkisacutacin, a new fibrinolytic & anti-platelet protein from Agkistrodon acutus venom
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                                                544; DB 6; I
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/codon_gtart=1
/product="agkiaacutacin_A chain"
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TWTDAESFCTKQVNGGHLV9IESSGEADFVGQLIAQKIKSAKIHVWIGLRAQNKEKQC
SIEWSDGSSISYENNIBEBSSKKCLGVHIETGFHKWENFYCEQQDPFVCEA" /tissue type="venom"

89. .547

/ince="consists of two heterologous subunits (A and B chains) linked by an inter-subunit disulfide bond; c-type lectin family member" Direct Submission
Submitted (23-APR-2002) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, School of
Life-Science, Huangshan Road, Hefei, Anhui 230027, China
Sequence update by submitter
On Apr 23, 2002 this sequence version replaced gi:6715112. 244 120 180 240 of 304 241 AGTTATGAGAATTGGATTGAAGAAGCAATCCAAAAGTGTCTTGGGGTGCACATAGAGACA 300 364 424 GGGTTTCATAAGTGGGAAATTTTTACTGTGAACAACAAGATGCTTTTTGTCTGGGAGGCA 360 09 484 544 420 604 School 185 GAAGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC TGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTCTATCGAAAGCTCCGGAGAAGCAGAC TGCACGAAGCAGGTGAACGGGGGGGATCTGGTCTCTATCGAAAGCTCCGGAGAAGCAAG TITGTGGGCCAGTIGATIGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGA CTGAGGGCTCAAAAGAAAAAGCAATGCAGCATAGAGTGGAGGGATGGCTCCAGGATC GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGGGCTTC AGTTATGAGAATTGGAAGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA Gaps TAGTCTGAAGATCCAGCTGATTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACCCCATCCC d (bases 1 to 733)
Cheng, X., Liu, J., Li, B.X.Y. and Qian, Y.
Direct Submission
Submitted (08-AUG-1999) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, Scho
Life-Science, Huangshan Road, Hefei, Anhui 230027, China
Yu, H.-X., Xiang, K.-J., Wang, Y. and Liu, J. 3; 733; 3 (bases 1 to 733)
Yu, H.-X., Xiang, K.-J., Wang, Y. and Liu, J.
A chain of agkisacutacin from Deinagkistrodon acutus Unpublished

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Submitted (06-JAN-2000) Tomohisa Ogawa, Tohoku University, Graduate School of Agricultral Science; 1-1, Tsutusmidori Amamiyamachi, Aoba-ku, Sendai 981-8555, Japan (E-mail:ogawa@biochem.cohoku.ac.jp, URL:http://www.agri.tohoku.ac.jp/hoozo/, Tel:81-22-717-8808, Fax:81-22-717-8807)
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TWADARSFCTKQVNGGHLVSIESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQC
SIEWSDGSSISYENWIEBESKKCLGVHKATGFRKWENFYCEQRDFFVCEA"
                                                                                                                                                                                        ABUJSBENG 656 bp mRNA linear VRT 23-MAY-2002 Deinagkistrodon acutus acp-a mRNA for anticoagulant protein A, complete cds.
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anticoagulant protein A.
Deinagkistrodon acutus
Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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                                           GCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGCCTAGCCT
                                                                                                                                                                                                                                                                                                                                                                       Tani, A., Ogawa, T., Nose, T., Nikandrov, N.N., Deshimaru, M., Chijiwa, T., Chang, C.C., Fukumaki, Y. and Ohno, M. Charatterization, primary structure and molecular evolution anticoagulant protein from Agkistrodon actus venom Toxicon 40 (6), 803-813 (2002)
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                                                                                                                                                                                                                                                                                                                                                 Viperidae; Crotalinae; Deinagkistrodon.
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1. .656
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/db_xref="GI:8980619"
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/codon_start=1
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AB036880
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/codon_start=1/2 A-chain"
/prodein_id="AAM22786.1"
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SIEWSDGSSISSYENWIEBESSKKCLGVHKATGFRKWBNFYCEQRDPFVCEA"
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Deinagkistrodon acutus clone 2100590 ACF 1/2 A-chain mRNA, complete
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TITGIGGGCCAGITGATIGCTCAGAAGATAAAGTCAGCCAAAAAICCAIGTCIGGAICGGA 180
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Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metacoa; Chordata; Caleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
Viperidae; Lo 497)
Yu, H., Xiang, K., Wang, Y. and Liu, J.
A. Chain of ACF 1/2 from Deinagkistrodon acutus
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Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAACCCTGCCTAGCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTCTCTGTA
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Direct Submission
Submitted (22-MAR-2002) Dept. of Biochemistry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .459
/note="C-type lectin family member"
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/mol_type="mRNA"
/db_xref="taxon:36307"
/clone="2100590"
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Pred. No. 9.9e-102;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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Ogawa, T. and Ohno, M.
Direct Submission
Submitted (24-JJJ-2000) Tomohisa Ogawa, Tohoku University, Dept.
Agricultural Science; 1-1 Tsutsumidori Amamiyamachi, Aoba-ku,
                                                                                                                                                                      GAAGGGCATTGCTACAAGGCCTTCGAAAATACAAGACCTGGGAAGATGCAGAAGACTC
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Charcterization and molecular evolution of an anticoagulant Unpublished
                                                                                                                  10;
                                                                                     Length 678;
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Pred. No. 2.3e-101;
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/product=fractor IX/factor X binding protein A chain"
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/db_xref="101:1402640"
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TREABRRVCFEQAKGAHLVSIESSGRADFVAQLVTQNMKRLDFYIWIGLRVQGKVKQC
NSEWDDGSSVSYENWIEAESKTCLGIEKETDFRKWVNIYCGQONPFVCEA"
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1 (bases 1 to 678)
Matsuzaki,R., Yoshiara,B., Yamada,M., Shima,K., Atoda.H and Morita,T.
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                                                                                         TGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTCTATCGAAAGCTCCGGAAGAAGCAGAC
                               GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGGCTTC
                                                                                                                                                                                  TITGIGGCCCATCTGATTGCTCAGAAGATAAAGTCCAGAAATCCATGTCTGGATCGGA
                                                                                                                    TTTGTGGGCCCAGTTGATTGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGA
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Location/Qualifiers
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         Indels
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/organism="Trimeresurus flavoviridis"
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facotr IX/factor X binding protein A chain.
Trimeresurus flavoviridis
Trimeresurus flavoviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                               491
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    Mismatches
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Trimeresurus flavoviridis mRNA for protein A chain, complete cds.
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/db_xref="taxon:88087"
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/trānslation="mgrfiftyvyfgllvyflslsgtgadfnoppgwsaydqvyquike
pknwddaerfcteqadgghlvsieskgerdfvaqlvsqniesvedhywtglrvqnkek
qcstewsdgssvsyenllelymrkcgaleretgfhkwinlgciqlnpfvckfppqc"
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-AUG-2002) Department of Nursing, Chang Gung Institute of Technology, 261, Wen-Hwa 1 Rd., Kwei-Shan, Tao-Yuan, Taiwan
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                                                                                                                                                                                                                                             Wang, W.-J., Ling, Q.-D. and Huang, T.-F.
Molecular structure and functional characterization of agglucetin, a tetrameric glycoprotein Ib-binding protein, from Formosan pit
            Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.

1 (Dases 1 to 661)

Wang, W.J. and Huang, T.F.

A novel terrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist
Thromb. Haemost. 86 (41, 1077-1086 (2001)
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/protein_id="AAN23125.1"
/db_xref="G1:23321261"
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                                                                                                                                                                                                                                                                                                                                                                    Wang, W.-J., Ling, Q.-D. and Huang, T.-F. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Deinagkistrodon
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159 c 183 g 152 t
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/db_xref="taxon:36307"
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al Similarity 79.6%;
437; Conservative
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RVCTEQAKGAHLVSIESSGEADFVAQLVTQNMKRLDFYTWIGLRVQGKVKQCNSEWSD
GSSYSYENWIEAESKTCLGLEKETDFRKWVNIYGGQNPFVCEA"
162 c 155 t 155 t
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Sendai, Miyagi 981-8555, Japan (E-mail:ogawa@biochem.tohoku.ac.jp,
Tel:81-22-717-8808, Fax:81-22-717-8807)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                        'product="factor XI/factor X binding protein A
                                                                                  /organism="Trimeresurus flavoviridis"
/mol_type="mRNA"
/db_xref="taxon=80807"
/issue type="venome gland"
/country="Japan:Kagoshima, Tokunoshima island"
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Pred. No. 6e-95;
0; Mismatches 82;
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db_xref="GI:12583677"
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77. .517
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Deinagkistrodon acutus
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Best Local Similarity 82.7%;
Matches 445; Conservative
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Unpublished
3 (bases 1 to 666)
Wang, W.-d., Ling, Q.-D. and Huang, T.-F.
Wang, W.-d., Ling, Q.-D.
Submitted (23-AUG-2002) Department of Nursing, Chang Gung Institute of Technology, 261, Wen-Hwa 1 Rd., Kwei-Shan, Tao-Yuan, Taiwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1.
/codon_start=1.
/product=#agglucetin-alpha 1 subunit precursor"
/protein_id="Amx131124.1"
/db_xref="G1:23321259"
/db_xref
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karayota, Metazooa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa; Serpentes, Colubroidea,
Viperidae, Crotalinae, Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of agglucetin,
             2 (bases 1 to 666)
Wang,W.-J., Ling,Q.-D. and Huang,T.-F.
Molecular structure and functional characterization of agglucetia tetrameric glycoprotein Ib-binding protein, from Formosan pit
                                                                                                 TTTGTGGGCCAGTTGATTGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGA
                                                                                                                                             TITGIGGCCCAGCTGGTCTCTGAGAACATGAAGAGATACGGGATCTATATCTGGATCGGA
                                                                                                                                                                                                      CTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC
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/note="platelet agglutination inducer; glycoprotein Ib
agonist"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist
Thromb. Haemost. 86 (4), 1077-1086 (2001)
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/mol_type="mRNA"
/db_xref="taxon:36307"
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Wang, W.J. and Huang, T.F.
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/protein_id="AAG1719.1"
/brotein_id="10441756"
/brotein_id="10441756"
/translation="WREFIESEFELLIVVELSLSGTGADCPSGWSSYEGHCYNIFHLFK
TWARAERFCRKQVKGAHLVSIESSEEDDFVAQLVSENWRRYGIYIWIGLRYRGKKQC
SSQWSDGSSVSYQNWIEAESKTCLGLQKETEFRKWFNIYCGERNPFVCEA"
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652
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1 (Dases 1 to 630)

Roo, B.H., Sohn, Y.D., Kim, D.S., Jang, Y.S. and Chung, K.H.

A novel cogulation factor Xa inhibitor from Korean snake (Agkistrodon halys) venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TGCACGAAGCAGGTGAACGGGGGGGCATCTGGTCTATCGAAAGCTCCGGAAAAGCAGAC 120
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                                                                              CATCCCCCAACCTGCCTAGCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTC
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Koo, B.H., Sohn, Y.D., Kim, D.S., Jang, Y.S. and Chung, K.H.
Direct Submission
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Pred. No. 1.5e-82;
0; Mismatches 66
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/organism="Gloydius halys"
/mol_type="mRNA"
/w_xref="taxon:8714"
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Gloydius halys
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Best Local Similarity 84.2%;
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/gene="HXNA"
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Sistrurus.
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Sistrurus miliarius
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Patent: WO 0214364-A 4 21-FEB-2002;
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Sequence 4 from Patent W00214364.
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
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Chen, Y.L., Hong, T.M., Chang, T. and Tsai, I.H.
Chen, Y.B., Hong, T.M., Chang, T. and Tsai, I.H.
Sequence and functional characterization of glycoprotein
Ib-binding protein from the venom of Deinagkistrodon acutus
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Chen, Y.L. and Tsai, I.H.
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Trimeresurus flavoviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosautia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.

1 (bases 1 to 681)
Shin, Y., Okuyama, I., Hasegawa, J. and Morita, T.
Molecular cloning of glycoprotein Ib-binding protein, flavocetin-A, which inhibits platelet aggregation
Thromb. Res. 99 (3), 239-247 (2000)
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164 c 182 g 165 t
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Pharmaceutical University, 2-522-1, Noshio, Kiyose, Tokyo 204-8588,
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Pred. No. 9.4e-78;
0; Mismatches 116; Indels
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/protein_id="AAN72438.1"
/db_xref="G1:25245561"
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/codon start=1
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/db_xref="taxon:88087"
/tissue_type="venom glands"
37. .513

    681
    organism="Trimeresurus"

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76.7%;
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Shin, Y., Okuyama, I.,
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/protein id="AAG42040.1"
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SKWSDSSKVSYENLVEPFSKKCFVLKKDTGFRTWENVYCGLKHVFMCKYLKPR"
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/translation="MGREIFYSFGLLVLFLSLSGTGAGLHCPSDWYYYDQHCYRIFNE
EMNWEDAEWPCTKQAKGAHLVSIKSAKEADFVAWMVTQNIESFSHVSIGLRVQNKEK
QCSTKWSDGSSVSYDNLLDLYITKCSLLKKETGFRKWFVASCIGKIPFVCKFPPQC"
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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Direct Submission
Submitted (27-JAN-1998) M. Leduc, Institut Pasteur, Unite des
Venins, 25 Rue du Dr Roux, 75724 Paris cedex 15, Paris, FRANCE
                                                                                                                                                                                                                                                                                                              Leduc,M. and Bon,C.
Cloning of subunits of convulxin, a collagen-like
platelet-aggregating protein from Crotalus durissus terrificus
CTCTGTAGCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGC
              617 CTCTGTAGCTGGATCTGGTTTTGCTGCTCCTGATGGGCCCAGAAGGTCCAATAAATTCTGC
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Pred. No. 5.4e-75;
0; Mismatches 123; Indels
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convulxin alpha; CVX alpha gene.
Crotalus durissus (tropical rattlesnake)
Crotalus durissus
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/protein_id="CAA76181.1"
/db_xref="GI:3367646"
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/brotein id="CAD35501.1"
/db_xref="G1:21530573"
/db_xraf="G1:21530573"
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Sistrurus.
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/mol_type="genomic DNA"
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Pred. No. 6.2e-75;
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Rattlesnake venom gland proteins
Patent: WO 0214364-A 10 21-FEB-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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AKGGHLVSIESDGEAAFVAQLVAENIKONKYDVWIGLRIQGEEKQCSTKWSDGSSVNY
ENLIKHATKKCFGLKKETGFRTWRNVHCTQQNLFMCKFPPEC"
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Sistrurus.
                         GAAGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC
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  Mismatches 110;
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/mol_type="genomic DNA"
/db_xref="taxon:8758"
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Sistrurus miliarius
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Rattlesnake venom gland proteins
Patent: WO 0214364-A 7 21-FEB-2002,
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/db_xref="GI:21530570"
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AX427207
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Location/Qualifiers
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/codon_start=1
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AUTHORS
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FEATURES

SOURCE

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                                                             Length 580;
                                      Score 285.8; DB 6; Lens.
Pred. No. 2.8e-74;
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Conservative
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                                                                                                                                                                                                                                                                                   December 8, 2003, 09:08:47; Search time 321 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES
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Result No. 1 2 2 3 3 4 4	Score 544 306.2 288 285.8 276.2	% Matchy 100 -0 -1 -1 -1 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0	Query re Match Length DB I Match Length DB I 721 24 25 32 725 24 25 50.8 632 24 25 50.8 648.9 601 22	DB 255 244 244 224 224 224 224	SUMMARIES SUMMARIES ABX93668 AAD22055 AAD22057 AAL42015 AAL42015 AACA9309	Description CDNA encoding Dein Pigmy rattlesnake Pigmy rattlesnake Pigmy rattlesnake Rorean adder snake Snake venom blood
- 00	226.4			21		DNA encoding a sna

US6489451-B1

DNA encoding the a Pigmy rattlesnake Pigmy rattlesnake Pigmy rattlesnake Pigmy rattlesnake Snake venom antith Rattlesnake venom Korean adder snake	Figmy rattlesnake Snake venom protei Pigmy rattlesnake CDNA encoding Dein Drosophila melanog Nucleotide sequenc	Drosophila melanog Human secreted pro Human secreted pro Human CDNA differe CDNA encoding colo Human Zlecl encodi Human lectin Zlecl CDNA encoding colo	Human pancreatic c Degenerate DNA enc Human Zfeta2 degen DNA encoding novel DNA encoding novel DNA encoding novel Sequence encoding	cDNA encoding colo Human reg cDNA. H Sequence of human Human colon associ Human colon associ Bovine pancreatic cDNA encoding colo
AAK99834 AAD32056 AAD32058 AAD32060 AAT11877 AAC611143 AAC61163	AAD32053 AAT64829 AAD32054 ABX93674 ABL27241 AAH28279	ABL27240 AAC59784 AAF24170 ABK83461 AAK46204 AAD27975 ABK46210	ABV97585 AAD00024 AAD37455 AAS67247 AAS66042 AAS64652	ABK46235 AAN91109 AAN81106 AAF75077 AAC77946 AAF75090 AAQ05300
22222122 44442314	24 17 25 23 23	62222222 64244244	22 23 23 23 11	2010 2010 2010 2010 4
64 4 4 8 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	483 716 453 454 10598	8 4 4 8	509 2949 2949 1221 1222 2581 441	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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ALIGNMENTS

ABX93668 standard; cDNA; 544 BP.

RESULT 1 ABX93668 ABX93668;

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Antithrombosis; ss; PCR; alpha chain; fibrin hydrolysis; blood clot; platelet aggregation; vaso-occulusive disorder; thromboembolic disorder; myocardial infarction; restenosis; cancer; neurodegenerative disease; angiopathic thrombosis; cerebral thrombosis; thromboangilis obliterans; ischaemic cerebral vascular disease; unstable angina; acute thrombosis; peripheral estenocardia; pulmonary embolism; deep vein thrombosis; oedema; peripheral arterial occulsion; stroke; atherosclerosis; inflammation; thrombosis.
                                                       cDNA encoding Deinagkistrodon acutus antithrombosis enzyme alpha chain.
                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Antithrombosis enzyme alpha chain"
                                                                                                                                                                                                                                                                                                                                                  /partial
/transl_except= (pos:244..246,aa:Lys)
/note= "No start codon given"
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                             (first entry)
                                                                                                                                                                                                                                                  Deinagkistrodon acutus.
                             02-JUN-2003
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N

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Bishop
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P-PSDB; AAE20179.
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                                                                                                                                                                                                                                                                                                                          composition is useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, angiopathic thrombosis, including myocardial infarction, restenosis, angiopathic thrombosis, ischaemic cerebral vascular thrombosis, ischaemic cerebral vascular thrombosis, unstable stenocardia, peripheral arterial occulsion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents cDNA encoding the Deinagkistrodon acutus antithrombosis enzyme alpha chain.
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                                                                                                                                                                                                                             The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.05 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro/kg. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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                                                                                                                                                 New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thrombosmbolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
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                                                                     SIU FUNG USTC PHARM CO LID.
                                                                                                                                                                                                           Example 3; Column 25-26; 19pp; English.
                        98US-0058740.
                                               97US-043886P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 544, Conservative
                                                                                                                 WPI; 2003-352116/33.
                                                                                           Cheng X;
                                                                                                                              P-PSDB; ABU08798
                                                                                                                                                                                     unstable angina
                                                                   (HEFE-) HEFEI
                        10-APR-1998;
                                              10-APR-1997;
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CCAACCTIGCCTAGCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTCTGTA
                                                               GCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAGTCAATAAATTCTGCCTAGCCTGA
                                                                                                 Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; gene; Zsnk3; ds.
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/product= "Mature Zsnk3 protein"
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/product= "Zsnk3 protein"
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weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tegas, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
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cagregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
platelet aggregation system as an educational tool in laboratory
practical kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The
polynuclectide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
proteins by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dicincisms to determine conformation or
faffinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein, Zsnk5 gene.
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Pred. No. 2.8e-80;
0; Mismatches 110;
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                                                              ; 2000US-225072P.
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20-DEC-2000; 2000US-356997P.
                                   2001WO-US25310
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practical kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The polynucleotide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or sequencing. The present sequence is Sistrurus miliarius venom gland protein, Zsnk4 gene.
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                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                           580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Korean adder snake venom salmorin A chain protein cDNA sequence
                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                 Sequence 580 BP; 154 A; 133 C; 163 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                       Score 285.8; DB 2
Pred. No. 1.2e-79;
0; Mismatches 97
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75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which
                                  CATCCCCCAACCCTGCCTAGCCACAATCTCTGCTATGCACCCT-TTGCTCAACGGATGCT
                                                                                                          CTCTGTAGCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGC
                                                                                                                                          CTCTGTGGCTGGATCTGGTTCTGCTGCTCCTGATGGGCCAGAAGGTCCAATAAATTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          rattlesnake; venom gland protein; blood coagulation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, set blood coagulation and platelet aggregation system, useful i rapy and diagnostics, or as tools in the study of genetics or
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not include start codon"
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/*tag= c
/product= "Mature Zsnk4 protein"
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platelet aggregation; gene; Zsnk4; ds
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/note= "CDS does no
/partial
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15-AUG-2000; 2000US-225489P.
15-AUG-2000; 2000US-225490P.
20-DEC-2000; 2000US-356997P.
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15-AUG-2000;
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sig_peptide mat peptide

Key

18-JUN-2002

AAD32057

AAD32057

Sheppard PO,

therapy

242 240 302

362 356

us-09-938-114-1.rng

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181 CTGAGGGCTCAAAACAAAGAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC 240
           302 GGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCGAGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the nucleotide and protein sequences of a salmorin protein derived from the venom of Korean adder. Salmorin protein is composed of an A chain and a B chain, and has inhibitory activity against fibrinogen clotting. The salmorin protein of the invention is useful for treating thrombosis, as it represses fibrinogen clotting potently by binding to prothrombin and thrombin so as to delay blood coagulation. The present cDNA sequence encodes the Korean adder salmorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
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                                                                                                                                                     /*tag= c
/note= "Mature Salmorin A chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 632 BP; 162 A; 140 C; 182 G; 148 T; 0 other;
                                                             /*tag= a
/product= "Salmorin A chain protein"
                                                                                                        /*tag= b
/note= "Signal peptide"
                              Location/Qualifiers
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halys brevicaudus
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80.0%;
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623..632
/*tag= e
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                                            137 ATTATCATAAGTGGGTCAATGTTTACTGTGGACAAAGAAATGCTTTGTCTGCGAGGCTT
                                                                                                                     GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence encodes the A chain of halyxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to halyxin, a novel protein with very strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snake, pit viper; venom; halyxin; anticoagulant; thrombogenesis;
thrombosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snake venom blood anticoagulant halyxin A chain coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 601 BP; 166 A; 133 C; 163 G; 139 T; 0 other;
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           168 GATCGGTATTGCTACAAGCCCTTCAAACAAGAGATGACCTGGGCCGATGCAGAGAGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kayahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding a snake venom derived protein.
                                                                                                                                                                                                                                                                    CTGAGGGTTCAAACAAAGGACAGCCAT-
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                                                                AGTTATGAGAATTGGAATTGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA 300
                                                                                                                                               301 GGGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCGAGGCA 360
CTGAGGGTTCGAGGCAAAAGAAGCAATGCAGCTCCCAGTGGAGCGATGGCTCCAGCGTC 359
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                                                                                                       AGTTATCAGAACTGGATTGAAGCAGAATCCAAAACGTGTTTTGGGCTGCAAAAAGAGACA
                                                                                                                                                                                         GAGTTTCGTAAGTGGTTTAATATTTACTGTGGAAACGAAATCCTTTCGTCTGCGAGGCA
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(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; snake venom; platelet binding inhibition; factors; Crotalus horridus horridus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single-chain antithrombotic peptide - obtained by cleaving an oligopeptide from snake venom to break inter-chain di:sulphide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii K, Kito M, Kobayashi T, Nagano M;
Yamamoto H, Yoshimoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligopeptide from snake venom to break inter-cha.
bonds but preserve intra-chain di:sulphide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snake venom antithrombotic oligopeptide cDNA
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66..515
                                                                                                                                                                                                                                                                                                                                                                                 AAQ89309 standard; cDNA; 690 BP
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(first entry)
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Best Local Simil
Matches 389; C
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28-NOV-1995
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Producing physiologically-active subunit peptides originating in polymer proteins by denaturation and specific separation, with lower antigenicity but improved solubility and stability, e.g. blood platelet-binding inhibitors
Yamamoto H;
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GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGGCTTC

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                                 This invention relates to a method for the production of a subunit peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its
                                                                                                                                                                                                                                                                           9
                                                                 subunit using a protein dematuring agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity on von willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents DNA encoding rattlesnake protein used in an example illustrating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 ACGCGACCACGTTAAGATCCGGCTGTGTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGTAGCTGGATCTGGTGGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGTAGCCGGATCTGGGTTTTCTGCTCCAGATGGGTCAGAAGATCCAATAAATTCTGCC
                                                                                                                                                                                                                                                                                                   GATCGGTATTGCTACAAGCCCTTCAAACAAGAGATGACCTGGGCCGATGCAGAGAGGTTC
                                                                                                                                                                                                                                                                                                                           TGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTATCGAAAGCTCCGGAAAGCAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                TTTGTGGACAATGTGCTCTCTATGCGAACAAAGAGTACCTCACACGTTATATCTGGATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GCTCCAGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTATGAGAATTGGATTGAAGAAGAATCCAAAAAGTGTCTTGGGGGTGCACATAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GACCCATTTGAATGTTTTATGGTGAGCAGAGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCCCCCAACCCTGCCTAGCCACAATCTCTGTTATGCACCCTTTGCTCAACGGATGCTC
                                                                                                                                                                                                                                                                                                                                                 Tectoggageagecgaaggegegearcretererereaaacegeceragaagearee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCGA----
                                                                                                                                                                                                                                                                           GAAGGCCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC
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                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding the antithrombotic wild-type rattlesnake protein.
                                                                                                                                                                                                                             21; Length 690;
                                                                                                                                                                                                                                                  126; Indels
                                                                                                                                                                                                    Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                          Score 226.4; DB 2
Pred. No. 7.2e-61;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAGGGTTCAAAACAAAGGACAGCCAT-
           Disclosure; Page 46; 51pp; Japanese.
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Thrombolytic; glycoprotein 1b-binding protein; snake venom; rattlesnake; antithrombotic; glycoprotein 1b; long half life; low antigenicity;
                                                                                                                                                                                                                                       "Antithrombotic wild-type rattlesnake protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a glycoprotein Ib-binding protein, originating from snake venom, comprising specific mutations and antithrombotic activity. Glycoprotein Ib-binding protein is used in a drug having antithrombotic activity. Glycoprotein Ib-binding protein has a high binding activity to glycoprotein Ib- a long half life/drug efficacy retention in blood, and low antigenicity. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCGGTATTGCTACAAGCCCTTCAAACAAGAGATGACCTGGGCCGATGCAGAGAGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents DNA of the wild-type rattlesnake protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein Ib-binding protein, useful for treating thrombosis, comprises specific mutations in protein originating from snake \( \)
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Pred. No. 7.2e-61;
0; Mismatches 126; Indels
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                                                                                                                                                     Location/Qualifiers
66..515
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Local Similarity 70.5%;
es 389; Conservative (
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                                                                                                          Crotalus horridus horridus
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/product=
                                                           drug efficacy; gene; ds
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Shimba N,
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Sequence 456 BP; 72 A; 31 C; 92 G; 66 T; 195 other;

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide can be used as standards or as unknowns
polymucleotide or polypeptide are also useful in identifying
proteins by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
then the protein cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
474
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                                                      CATCCCCCAACCCTGCCTAGCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTC
                                                                                     TCTGTAGCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGCC
                                                                                                                                                                                                                                                                                                                                      Pigmy rattlesnake venom gland protein Zsnk3, degenerate nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                  rattlesnake; venom gland protein; blood coagulation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, affect blood coagulation and platelet aggregation system, useful itherapy and diagnostics, or as tools in the study of genetics or
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2000US-225489P.
2000US-225490P.
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P-PSDB; AAE20179.
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14-AUG-2000;
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protein Zank3, degenerate nucleic acid

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                                                                                                                                                                                                                                                                                        301 GGGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCGAGGC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gland proteins, which system, useful in of genetics or
                                                               1 GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC
                                                                                                                                             TITIGEGGCCAGTIGATIGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pigmy rattlesnake venom gland protein Zsnk4, degenerate nucleic acid.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rattlesnake; venom gland protein; blood coagulation; therapy;
                            ö
       Length 456;
   ; Score 186.6; DB 24; Length; Pred. No. 2.1e-48; 86; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New pigmy rattlesnake (Sistrurus miliarius) venom affect blood coagulation and platelet aggregation therapy and diagnostics, or as tools in the study
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    34.3%;
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14-AUG-2000; 2000US-225087P.
15-AUG-2000; 2000US-225489P.
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Query Match
Best Local Similarity 47.19
Matches 169; Conservative
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        agglegation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory polypeptides are also useful as an educational tool in laboratory practical kits for courses related to genetics and molecular biology, protecin chemistry and antibody production and analysis. The polymucleotide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or sequencing. The present sequence is Sistrurus miliarius venom gland
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blood coagulation and
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                                                                                                                                                                                                                                                                                 32.2%; Score 175; DB 24; Length 4 45.7%; Pred. No. 9.3e-45; tive 85; Mismatches 109; Indels
                                                                                                                                                                                                                                                Sequence 432 BP; 91 A; 34 C; 84 G; 55 T; 168 other;
which affect
                                                                                                                                                                                                                 protein Zsnk4, degenerate nucleic acid.
polypeptides,
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Best Local Similarity 45.7%
Matches 163; Conservative
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15-AUG-2000;
15-AUG-2000;
20-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet pagregation system. The polypeptides, which affect blood coagulation and platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory practical kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The polympetide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal ages, mass spectromeetry, circular dichroism to determine conformation or the states are also used as determined or as a succession of the symmetry of circular dichroism to determine conformation or the states, mass spectromeetry.
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                                                                                                                                                                                                                     New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      affinity chromatograph, columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland
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AAC61143 standard; DNA; 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 CAGGCATAGTTTGAAGATCCAGCTGAGTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACAT 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAGGGCTCAAAACAAAGGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 ACTAATAACAAATGGAGGAGTAGGAGCCTGCAGAATGGAGGCATATTTCGTCTGGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -AGGCATAGTCTGAAGATCCAGCTGATTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TITGIGGCCAGTIGATIGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGTGGTCAAGCTGGCCTTCCA----AAATTTTGGCCACGGTATTTCTGGATGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĊTGAG-----CAATGTCTGGAATCAATGCAGCTGGCAATGGAGCAGTGCTGCCAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTATGAGAATTGGAAGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCCCCAACCCTGCCTAGCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CACCCTTCGCTCAATGGATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTAGCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGCC
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                        The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence
                                                                                                                                                                                 Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCG
                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                          Query Match 26.5%; Score 144; DB 22; Length 633; Best Local Similarity 63.4%; Pred. No. 6.7e-35; Matches 350; Conservative 0; Mismatches 140; Indels 6;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                      Sequence 633 BP; 179 A; 142 C; 157 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                              0; Mismatches 140;
                                                                                                                                  ğ
                                                                                                                                    Son
                                                                                                                                  BH,
                                                                                                                                  Koo
                                                                                                                                                                                                   Claim 1; Page 11; 21pp; Korean.
                                                                                                                                                                                                                                                                   encodes the B chain of halyxin.
                                                                     29-JUN-2000; 2000KR-0036591
                                                                                         99KR-0025105
                                                                                                                                 Kim DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGCCTGAAAAA 544
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                                                                                                              CO LTD
                                                                                                                                                    2001-637330/73.
                                                                                                                                  Jung GH,
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
          Agkistrodon halys.
                                                                                                                                                               P-PSDB; AAM51544
                                                                                                              (BIOB-) BIOBUD
                             KR2001049671-A
                                                                                         29-JUN-1999;
                                                  15-JUN-2001
                                                                                                                                 YS,
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94 TCTATCGAAAGCTCCGGAGAAGCAGACTTTGTGGGCCAGTTGATTGCTCAGAAGATAAAG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 TACCTCACACGTTATATCTGGATTGGACTGAGGGTTCAAAACAAAGGACAGCCATGCTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ89308 is a snake venom cDNA used in the prepn. of AAQ89309, which encodes AAR71981 a snake venom oligopeptide. From this oligopeptide claimed antithrobtic peptides where derived, the peptides had the advantage of avoiding significant thrombocytopenia when administered at the minimun dose, for in vivo inhibition of platelet von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGACCTGGACAGAGAGAGGTTCTGCACGAAGCAGGTGAACGGGGGGCATCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ATGACTTGGGCCGATGCAGAGGTTCTGCTCGGAGCAGGCGAAGGCGGGCATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                            snake venom; platelet binding inhibition;
Crotalus horridus horridus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single-chain antithrombotic peptide - obtained by cleaving an oligopeptide from snake venom to break inter-chain disulphide bonds but preserve intra-chain disulphide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagano M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 272 BP; 72 A; 60 C; 77 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102.6; DB 16;
Pred. No. 5e-22;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                          Snake venom antithrombotic oligopeptide cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kito M, Kobayashi
, Yoshimoto R;
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                      AAQ89308 standard; cDNA; 272 BP.
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Best Local Similarity 72.9%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-JP01555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0236975
                                                                                                                                                                                                                                                                                                                Crotalus horridus horridus
                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                         peptide;
factors;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii K, K
Yamamoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO KK.
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                                                                                                                                                                                                                                       Antithrombotic von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                           WO9508573-A1
                                                                                                                   25-MAR-2003
28-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1995,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukuchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka A,
                                                                      AAQ89308;
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AAQ89308
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AAC61143;

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TCTATCGAAAGCTCCGGAGAAGCAGACTTTGTGGGCCAGTTGATTGCTCAGAAGATAAAG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TACCTCACGTTATATCTGGATTGGACTGAGGGTTCAAAACAAAGGACAGCCATGCTCC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subunit using a protein denaturing agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which removing the agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity on von Willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents a method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a method for the production of a subunit peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 AAGACCTGGACAGATGCAGAGGTTCTGCACGAAGCAGGTGAACGGGGGGCATCTGGTC 93
                                                                                                                          Subunit peptide production; snake venom; rattlesnake; thrombolytic; ds; von Willebrand's factor; blood platelet-inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGACTTGGGCCGATGCAGAGGTTCTGCTCGGAGCGCGAAGGCCGGGCATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing physiologically-active subunit peptides originating in polymer proteins by denaturation and specific separation, with lower antigenicity but improved solubility and stability, e.g. blood platelet-binding inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Pred. No. 5e-22;
0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 272 BP; 72 A; 60 C; 77 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                       Kayahara T,
                                                                                      Rattlesnake venom related DNA SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 45; 51pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                       Kito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.9%;
Best Local Similarity 72.9%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000WO-JP02127
                                                                                                                                                                                                                                                                                                                                99JP-0096073
                                                   07-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                       Fukuchi N, Kageyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-664985/64
                                                                                                                                                                                                                   WO200059926-A1
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                                                                                                                                                                                                                                                                                                                                02-APR-1999;
                                                                                                                                                                                                                                                         12-OCT-2000.
                                                                                                                                                                                Synthetic.
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Search completed: December 8, 2003, 11:08:47 Job time: 323 secs

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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FASESEQ for Windows 2.0
SOFTWARE: FASESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFICATION - CURNOWN>
FILING DATE: -UNKNOWN>
FILING DATE: -UNKNOWN>
FILING DATE: -CUNKNOWN>
FILING DATE: -CUNKNOWN>
RIGHTON NUMBER: -SUNKNOWN>
REGISTRATION NUMBER: 38,673
REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 97071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISCIS:
LENGTH: 544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-058-740-1
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Sequence 7, Appli
Sequence 6, Appli
Sequence 14, Appl
Sequence 12, Appl
Sequence 3, Appli
Sequence 3, Appli
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2, Appli
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1, Appli
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Sequence 5, Appli
Patent No. 5514582
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Sequence 2, Appli
                                                                                                  December 8, 2003, 10:25:43; Search time 79 Seconds (without alignments) 3039.398 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15,
                                                                                                                                                                                       544
1 GAAGGCATTGCTACAAGGT.....AITCTGCCTAGCCTGAAAAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
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(GGTZ 6/ptodata/1/ina/5A COMB.seq:*

(GGTZ 6/ptodata/1/ina/5B COMB.seq:*

(GGTZ 6/ptodata/1/ina/6A COMB.seq:*

(GGTZ 6/ptodata/1/ina/6B COMB.seq:*

(GGTZ 6/ptodata/1/ina/PCTUS COMB.seq:*

(GGTZ 6/ptodata/1/ina/PCTUS COMB.seq:*

(GGTZ 6/ptodata/1/ina/PCTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-612-840A-7

US-08-232-463-14

US-09-058-740-12

US-09-058-740-12

US-09-412-554A-3

US-08-454-557C-32

US-08-450-672-32

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US-09-461-325-42
US-08-340-539A-5
US-08-461-592B-5
5514582-1
US-08-513-278-1
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US-08-729-103-2
US-08-468-413-1
US-09-162-508-1
PCT-US95-07169-1
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                                                                                                                                                                                                                                                                                                 569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                          IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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	56	31.2	5.7	46819	4	US-09-453-702B-72		
υ	30	30.8	5.7	5261	' -	US-08-045-806-3	Seguence	3 Appli
U	31	0	5.7	5261	Н	US-08-366-051B-3	Sequence	3, Appli
U	32	30.6	5.6	280	9	5198345-11	Patent No.	. 12
	33	30.6	5.6	289	m	US-09-007-005-17	Sequence 17, Appl	
	34	30.6	5.6	289	٣	US-09-244-796-17	Sequence	17, Appl
υ	35	30.6	2.6	289	9	5198345-18	Patent No.	
	36	30.4	5.6	747	7	US-08-401-530A-1	Sequence	1, Appli
	37	30.4	5.6	2325	7	US-08-714-677-3	Sequence	3, Appli
	38	30.4	5.6	2325	~	US-08-393-540-3	Sequence	
	39	30.4	5.6	2325	7	US-08-714-537-3	Sequence	
	40	30.4	5.6	3073	N	US-08-714-677-11	Sequence	11, Appl
	41	0	5.6	3073	7	US-08-393-540-11	Sequence	
	42	\circ	5.6	3073	~	US-08-714-537-11	Sequence	
\$	2	0	5.6	762	~	US-08-822-261-2	Sequence	
	44	o.	2.6	762	4	US-09-226-852-2	Sequence	7
υ	45	30	5.5	406	4	US-09-556-877-50	Sequence	
						ALIGNMENTS		
RES	RESULT 1							
ns-	350-60	US-09-058-740-1			0			
<i>α</i> α.	sequence 1, Patent No.	sequence 1, Application Us/U9U58/4U Patent No. 6489451	Applicat 6489451	lon US/) V	58 / 4 0		
	GENE	GENERAL INFORMATION:	RMATIO	 				
		APPLICANT:		Chun Wang,	Д.	~		
•-			J.	ng Liu,	Ë	Jing Liu, Li-Wen Niu, Wan-Zhi Huang,		
•-			ZÞ	en-Yu X	'n,	Zhen-Yu Xu, Dan Luo, Lian-Di Kang,		
•-			J.	Jin-Guo D	ing	, Fang Rong, Yan		
٠.				Hui-Ran C	Chen			
		TITLE C	OF INVE	NTION:	AN ANT	INVENTION: AN ANTITHROMBOSIS ENZYME FROM VIEWIGE OF ACKIETED AND ACKIETED OF ACKIETED ACKIETED	M THE SNAKE	
- •		GGGWITH	NAV	TENCEC.	4 5	5		
		CORRESE	CORRESPONDENCE ADDRESS:	E ADDRE	SS:			
		AI	ω	E: Lyon	48	Lyon		
		S	STREET:	633 West Fifth	بتا	ifth Street		
				Suite 4700	700			
	1	ฮ	CITY: Los Angeles	s Angel	8			

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61 TGCACGAAGCAGGTGAACGCGCCATCTCGTCTCTATCGAAAGCTCCGGAGAAGCAGAC
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           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Crotalus horridus horridus
FastSEQ Version 1.5
                                                                                                                                                                                                                   TELEPHONE: 703-413-3000
TELEPAX: 703-413-220
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
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Matches 389; Conservative
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ORIGINAL SOURCE
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; Sequence 7, Application US/08612840A
; Patent No. 5856126
; GENERAL INFORMATION:
APPLICANT: PUNCHI, Nacyuki
APPLICANT: NATAMOTO, Hiroshi
APPLICANT: NATO, Worikazu
APPLICANT: TANAKA, Akiko
; APPLICANT: TOSHIMOTO, ROSHIMOTO
; APPLICANT: TOSHIMOTO, PEPTIDE HAVING ANTI-THROMBUS
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spiver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 544;
                                                  0; Indels
             Score 544; DB 4; L
Pred. No. 1.3e-164;
O; Mismatches O;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 544; Conservative 0
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                                                                                                                                                                                                                                                                                                                                            ADDRESSEB: Oblon, Spivak, McClelland, Maier & Neustadt, P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                                APPLICANT: KOBAYASHI, TSUYOSHI
APPLICANT: YOSHIMOTO, RYOTA
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.9%; Score 102.6; DB 2; Length 272; 72.9%; Pred. No. 2.6e-23; ive 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAPELICATION NUMBER: US/08/612,840A FILING DATE: 20-MAR-1996 CLASSIPICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 5-236975 FILING DATE: 22-SEP-1993 ATTORNEY/AGENT INFORMATION: NAME: NO. 5856126man F. Oblon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crotalus horridus horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
                  Sequence 6, Application US/08612840A Patent No. 5856126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                FUKUCHI, Naoyuki
YAMAMOTO, Hiroshi
NAGANO, Mitsuyo
KITO, Morikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-413-300
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 base pairs
                                                                                                                                                                           TANAKA, Akiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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ORGANISM: Cro
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JS-08-612-840A-6
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                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                 APPLICANT:
                                                                                                                                                      APPLICANT:
                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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71 AGGTGAACGGGGGCATCTGGTCTTATCGAAAGCTCCGGAGAAGCAGACGTTGTGGGGCC 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 AAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATCAGTTATGAGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 GCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTCTGCACGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Conservative 222; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%; Score 58.4; DB 1; Best Local Similarity 6.2%; Pred. No. 2e-08; Matches 26; Conservative 222; Mismatches 168:
                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTOCNEY/AGENT INCEMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                        Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 683-4109
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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214 A 214
                                     187 A 187
                                                                                                                    US-08-232-463-14/c
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99 GAAGGCCATTGCTACAAGCCCTTCGATGAACCTAAGACCTGGGCAGATGCAGAGAAATTC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 AARCCNGTNTGYGGNWSNGAYGGNGARTTYTAYGARAAYCAYTGYGARGTNCAYMGNGCN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 GGCCAGTTGATTGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGACTGAGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 GCTCAAAACAAAGAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATCAGTTAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression and Detection
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Degenerate oligonucleotide sequence encoding the OTHER INFORMATION: zfsta2 polypeptide of SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 GAGAATTGGATTGAAGAATCCAAAAAGTGTCTTGGGGTGCACATA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/08454557C

Sequence 32, Application US/08454557C

GENERAL INFORMATION:

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression

TITLE OF INVENTION: 0.2 Alzheimer's Disease

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 34.6; DB 4; Length 2; Pred. No. 0.53; 43; Mismatches 117; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCATION: (1)...(2949)
CTHER INFORMATION: Each N is independently any nucleotide.
US-09-412-554A-3
                                                                                                                                                                                                                                                                                                        APPLICANT: Conklin, Darrell
APPLICANT: Ellaworth, Jeff L.
TITLE OF INVENTION: FOLLISTATIN RELATED PROFEIN ZFSTA2
FILE REFERENCE: 98-50
     20;
                                                                                                                                                    159 recacaacaacacaaaagecaeccarcre 188
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/412,554A CURRENT FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                  61 TGCACGAAGCAGGTGAACGGGGGGCATCTG
                                                                                                                                                                                                                                                 Sequence 3, Application US/09412554A Patent No. 6355788
     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.8%
Matches 68; Conservative
     70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: variation
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-454-557C-32
                                                                                                                                                                                                             RESULT 6
US-09-412-554A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
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     Matches
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                                                                                                                                    251 ATTGGATTGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACAGGGTTTCATA 310
                                                                                                              311 AGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCGAGGCATAGTCTGAAG 370
                                                                                                                                                                                                               371 ATCCAGCTGATTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACCCCATCCCCCAACC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE VENOM OF AGKISTRODON ACUTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 4; Length 454;
Pred. No. 6.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and Hui-Ran Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3...440 "N" stands for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Chen, Anthony C. REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3...440

OTHER INFORMATION: "N" stands

Maa" stands for any amino acid.
US-09-058-740-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: «UNKNOWIN-
FILING DATE: «UNKNOWIN-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (213) 489-1600
                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09058740 Patent No. 6489451 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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Best Local Similarity
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us-09-938-114-1.rni

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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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         20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-340-426D-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: OF Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ACTGCTACTACTTTAATGAAGACCGTGAGACCTGGGTTGATGCAGATCTCTATTGC---C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AGCAGGTGAACGGGGGGCATCTGGTCTTATCGAAAGCTCCGGAGAAGCAGACTTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 GCCAGTTGATTGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGACTGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 CCTCACTGAT --- TAAGGAGAGTGGCACTGATGACTTCAATGTCTGGATTGGCCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 CTCAAAACAAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATCAGTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AGICCIGGGCAITGGAGCCCCCAAGCAGTGITAATCCIGGCTACTGTGIGIGAGCCTGACCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 TAGAGACAGGGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 CAAGCACAGGATTCCAGAAATGGAAGGATGTGCCTTGTGAAGACAAGTTCTCCTTTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 ATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTCTGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.2; DB 2; Length 590;
Pred. No. 0.32;
0; Mismatches 148; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                     0609.3840003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 32, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
TELEFONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                      FILING DATE: 3: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 190;
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Fatent No. 594888e
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
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                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
ATTORNEY: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0609.3840002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,20.
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.3%; Score 34.2; DB 2; I Best Local Similarity 52.1%; Pred. No. 0.32; Matches 190; Conservative 0; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAATTGGATTGAAGAAGAATCCAAAA-----
                                                                                                                                                                                                                                                                               NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application PC/TUS9517111A GENERAL INFORMATION:
                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 590 base pairs
nucleic acid
                                                                   COMPUTER READABLE FORM:
3: D.C.
FRY: U.S.A.
20005-3934
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TOPOLOGY:
US-08-450-673C-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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68 AGCAGGTGAACGGGGGGATCTGGTCTCTATCGAAAGCTCCGGAGAAGCAGACTTTGTGG 127
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APPLICANT: Dieckgraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
FILE REFERENCE: 04255.75314
FILE REFERENCE: 04255.75314
CURRENT APPLICANTON NUMBER: US/09/146,969
CURRENT FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.32;
; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%; Score 34.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09146969
Patent No. 6228585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.1%;
                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 590 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 190; Conservative
                                                                       COMPUTER READABLE FORM:
1: D.C.
RY: U.S.A.
20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 GCGAG 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: both
                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
TELEFAX: (2
                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-17111A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-146-969-1
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Tue, Dec . 9 09:26:53 2003

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Query Match
Best Local Similarity
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-468-413-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 - CCATGACCCCAAAAGAACGCCGCGCTGGCACTGGAGCAGTGGGTCCCTGGTCTCCTACA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 GCCAGTIGATIGCICAGAAGAIAAAGICAGCCAAAAICCAIGIGIGIGGAICGGACIGAGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 CTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATCAGTTATG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AGTGTCTTGGGGTGCACA 292
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                                                                                                                                                                                                                                                                                                                                                 Score 32.6; DB 3; Length 777;
Pred. No. 1.2;
0; Mismatches 149; Indels 27; Gaps
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Sequence 2, Application US/08729103

Patent No. 5837841

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: INCYCE Pharmaccuticals, Inc.

STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 AGAATIGGATIGAAGAAGAATCCAAAA---
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PSATESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
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REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0138 US
TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 777
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 51.8%
Matches 189; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                  TYPE: DNA; ORGANISM: Homo sapiens
US-09-146-969-1
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 GCGAG 357
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254 ATTGCTATGGTTACTTCAGGAAGCTGAACTGGTCTGATGCCGAGCTCGAGTGTCAGT 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 CTTACGGAAACGGAGCCCACCTGGCATCTTGAGGTTTAAAGGAAGCCAGCACTAG 373
                                                                                                                                                                                                                                                                                                                                                                                                              8 ATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGGCTTCTGCACGA 67
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                 61; Indels
                                                                                                                                                                                                                                                                                                             Score 32.4; DB 2;
Pred. No. 1.2;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08468413
Patent No. 5861494
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,413
FILING DATE: 06 JUN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 294-1704
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  6.0%;
53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                     LENGTH: 614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                               69; Conservative
                                                                                                                                                              MOLECULE TYPE: CDNA
| IMMEDIATE SOURCE:
| LIBRARY: COLNFET02
| CLONE: 1310334
| US-08-729-103-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 GCCAGTTGAT 137
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STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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289 CTTACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AGCAGGTGAACGGGGGGCATCTGGTCTCTATCGAAAGCTCCGGAGAAGCAGCACTTTGTGG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGGGCTTCTGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 ATTGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 32.4; DB 5; 33.1%; Pred. No. 1.7;
                                                                                                                                                                                Sequence 1, Application PC/TUS9507169
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CRECHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: December 8, 2003, 12:41:19 Job time: 81 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325800-389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/07169
FILING DATE: 06 JUN 95
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFRERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Conservative
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                                       128 GCCAGTTGAT 137
                                                                                349 CAGAGTACAT 358
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                                                                                                                                                                                                                                                                                                                                                                                             STATE: NEW JERSEY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINEAR
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CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    07068
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PCT-US95-07169-1
                                                                                                                                             RESULT 15
PCT-US95-07169-1
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                                                                                                                                                    68 AGCAGGTGAACGGGGGGGCATCTGGTCTTATCGAAAGCTCCGGAGAAGCAGAAGTTTGTGG 127
                                                                                                                                                                                                                                               289 CTTACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AGCAGGTGAACGGGGGGGATCTGGTCTCTATCGAAAGCTCCGGAGAAGCAGACTTTGTGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 ATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGACTTCTGCACGA 67
                                                                                                                     8 ATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTCTGCACGA
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0
                                       6.0%; Score 32.4; DB 2; Length 1114; 53.1%; Pred. No. 1.7;
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                                                                              61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1. Application US/09162508
Fatent No. 6080722
GENERAL INFORMATION:
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CRCCHI, STEWRAT & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,134
ER: 325800-447
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,508
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,413
FILING DATE: 06 UIN 95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32
TELECOMUNINICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1114 BASE PAIRS
TYPE: NUCLEIC ACID
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SINGLE
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                                                                                                                                                                                                                                                                                                                                  349 CAGAGTACAT 358
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STATE: NEW JERSEY
COUNTRY: USA
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E: CDNA
                                  Query Match
Best Local Similarity
Matches 69; Conserv
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Matches 69; Conserv
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US-09-162-508-1
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US-08-468-413-1
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December 8, 2003, 12:02:04; Search time 346 Seconds (without alignments) 5225.543 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGGCATTGCTACAAGGT......ATTCTGCCTAGCCTGAAAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12. (cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2. (cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

3. (cgn2_6/ptodata/2/pubpna/US06_BWF_PUB.seq:*

3. (cgn2_6/ptodata/2/pubpna/US06_BWF_PUB.seq:*

4. (cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5. (cgn2_6/ptodata/2/pubpna/US08_BWF_PUB.seq:*

6. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

7. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

11. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

12. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

13. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

14. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

15. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

16. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

17. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

19. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

17. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

18. (cgn2_6/ptodata/2/pubpna/US08_UBW_PUB.seq:*

19. (cgn2_6/ptodata/2/pubpna/US08_UBW_PUB.seq:*

19. (cgn2_6/ptodata/2/pubpna/US08_UBW_PUB.seq:*

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13. (cgn2_6/ptodata/2/pubpna/US08_UBW_PUB.seq:*

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17. (cgn2_6/ptodata/2/pubpna/US08_UBW_PUB.seq:*

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19. (cgn2_6/ptodata/2/pubpna/US08_UBW_PUB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Description	Segmence 1	Segmenter	Segmence	Semience	Secretary	Secretarion	Secretarion	out to be	Portaines	Segment	Segmente	Sequence	Seguence	eduence	sednence	Sequence
0	US-09-938-114-1	JS-09-929-230-4	JS-10-226-420-4	JS-09-929-230-10	JS-10-226-420-10	US-09-929-230-7	JS-10-226-420-7	2-89-69-8I	9-052-656-51-SI	JS-10-226-420-6	JS-09-929-230-9	TS-10-226-420-9	TS-08-838-13	CL 0CA 2CC 01-01	77-074-077-07-07	JS-09-929-230-1
G E	11	10	13	10	13	10	13	10	10	13 1	101				1	10
% Query Match Length DB	544	721	721	725	725	580	580	690	456	456	432	432	474	474	F (F	483
% Query Match	100.0	56.3	56.3	52.9	52.9	52.5	52.5	41.6	34.3	34.3	32.2	32.2	30.5	30.5		15.1
Score	544	306.2	306.2	288	288	285.8	285.8	226.4	186.6	186.6	175	175	166	166		4.78
Result No.	н	7	Э	4	Ŋ	9	7	80	6	10	11	12	13	14	1 -	CT

Sequence 1. Appli	'n	'n	quence 30.	ď	175		1755.	۳,	Sequence 179264,		\vdash	176	1761,	2993,	ю.	178	178	178	11,	40,	24,	1778	1778	177		1756,	1756,	346,	
US-10-226-420-1	US-09-929-230-	US-10-226-420-3	726-		US-09-920-300A-17		US-10-033-528-175	US-09-801-		14 US-10-027-632-179264	US-09-920-300A	US-10	US-10-033-528-1	US-10-060	US-10-013-136-3		US-10-099-926-1786	US-10-033-528-178		US-09-925-301-340	US-09-997-003-24	US-09-920	US-10-099-926-1778	US-10-033-528-1778	US-09-920-300A-1756	-10-099-926-	US-10-033-528-1756	US-10-184-644-346	US-10-184-634-346
13	10	13	σ	14	10	13	14				10	13	14	15	15	10	13	14				10				13	Н	15	15
483	453	453	1597	1597	498	498	498	492	1223197	1223197	461	461			2949	493	493	493	800	843	843	585	585	585	593	593	593	671	671
15.1	11.8	11.8	6.8	6.8	6.7	6.7	6.7	9.9	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.3	6.3	6.3	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2
82.4	64.2	4.		36.8	36.4	36.4	36.4	36	•	ď.	4.	4.	34.8	•	4.	34.2	٠	٠		٠	•		•		٠ س	33.8	ش	<u>п</u>	
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ALIGNMENTS

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REGULT 1

US-09-938-114-1

US-09-938-114-1

Sequence 1, Application US/09938114

Sequence 1, Application No. US20030022350A1

Publication No. US20030022350A1

GENERAL INFORMATION:

APPLICANT: Chun Wang, Banjamin XX Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Jing Liu, Li-Wen Nay Liu and Hui-Ran Chen

TITLE OF INVENTION: AN ANTITHEOMBOSIS ENZYME FROM THE SNAKE, VENOW OF AGKISTRODON ACUTUS

NUMBER OF SEQUENCES: 1

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

COURTRY: U.S. Angeles

STATE: California

COUNTRY: U.S. Angeles

STATE: California

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/058,740

FILING DATE: -SIA-ANG-2001

CLASSIFICATION NUMBER: 09/058,740

FILING DATE: -CURNOWN-

ATTORNEY AGRET INFORMATION:

NAME: Chen, Anthony C.

REGISTRATION NUMBER: 38,673

REFERENCE/DOCKET NUMBER: 233/298
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56.3%;
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           Sistrurus miliarius
        GRGANISM: Sistrurus miliar
FEATURE:
NAME/KEY:
LOCATION: (91)...(546)
NAME/KEY: misc_feature
LOCATION: (0)...(0)
GOTHER INFORMATION: Zsnk3
US-09-929-230-4
                                                                                                                                                                                       Conservative
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US-10-226-420-4
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LOCATION: (91)...(546)
                                                                                                                                                                        Similarity
                                                                                                                                                        Query Match
Best Local Simi
Matches 365;
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Sequence 4, Application US/09929230

Patent No. US202020161203A1

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Sheppard, Paul D.

TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS

TITLE REPERENCE: 00-72

CURRENT APPLICATION NUMBER: US/09/929,230

CURRENT FILING DATE: 2001-08-13

SOFTWARE: FactSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 721
                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION
                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 base pairs
                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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     Length 721
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Score 306.2; DB 10;
Pred. No. 5e-94;
0; Mismatches 98; ]
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                                             370 CTGAGGATTCAAAACAAAGGACAGCAATGCAGCACGAAGTGGAGCGGTGGTCCAGCGTC
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; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION UNBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 725
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ORGANISM: Sistrurus miliarius
FEATURE:
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LOCATION: (88)...(561)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Zsnk5
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   721;
   DB 13; Length
Query Match 56.3%; Score 306.2; DB 13; Length Best Local Similarity 78.8%; Pred. No. 5e-94; Matches 365; Conservative 0; Mismatches 98; Indels
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Fatent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Blahop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION UNMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 725
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OTHER INFORMATION: Zsnk5
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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      CTGAGGGCTCAAAACAAAGAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC
                                                                        AGTTATGAGAATTGGAATTGAAGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA
                                                                                           TCTGTAGCTGGATCTGGTGTTGCTGCTCCTGATGGGCCGGAAG--TCAATAAATTCTGCC
                                                                                                                                                                                                        --GGCATAGTCTGAAGATCCAGCTGATTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACCC
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Fublication No. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Bishop, Paul O.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION UNMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
SEQ ID NO 7
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Zsnk4
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LOCATION: (3)...(434)
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US-10-226-420-7
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US-10-226-420-7
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                                                                                  CTGAGGATTCAAAACAAAGGACAGCAATGCAGCACGAAGTGGAGCGATGGCTCCAGCGTC
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APPLICANT: Bishop, Paul O.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION WUMBER: US/09/929,230
CURRENT APPLICATION WUMBER: US/09/929,230
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 580
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75.2%; Pred. No. 4.4e-87;
ive 0; Mismatches 97
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LOCATION: (3)...(434)

NAME/KEY: misc feature
LOCATION: (0)...(0)

COTHER INFORMATION: Zsnk4
US-09-929-230-7
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Matches 413; Conservative
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US-09-929-230-7
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18		Sequence 6, Application US/09929230
Db 243 CTGAGGATTCAAGGCGAAGAATGCAGCACGAAGTGGAGCGATGGCTCCAGCGTC 302 Qy 241 AGTTATGAGAATTGGATTGAAGAACCCAAAAAGTGTTTTGGGCTGCACATAGAGCA 300 Db 303 AATTATGAGAACTGATTAAACATGCGACCAAAAAGTGTTTTGGGCTGAAAAAAGACA 362 Qy 301 GGGTTTCATAAGTGGAGAATTTTTACTGTGAACAAAAAGTTTTGGCTGAAAAAAGAAA 362 Qy 302 GGGTTTCATAAGTGGAGAATTTTTACTGTGAACAAAAAAATTTTTTTT	QY 475 TCTGTAGCTGGATCTGGTTGCTGCTCCTGATGGGCGGGAAGTCAATAAATTCTGCC 532 Db 512 TCTGTAGCTGGATCTGGTTCTGCTGCTCCTGATGGGCCAGAAGGTCCAATAAACTCTTCC 571 QY 533 TAGCCTGAA 541 Db 572 TAGCCTGAA 580 RESULT 8 US-09-669-763-2 Sequence 2, Application US/09969763	PRICARIA INFORMATION: APPLICANT: WINCHI, MORINAL APPLICANT: WINCHI, MORINAL APPLICANT: WINCHI, MORINAL APPLICANT: WANAHAN, TRAKSHI APPLICANT: SITIKAMA, KOHIC APPLICANT: SONOGHISA APPLICANT: SONOGHISA APPLICANT: WANAHAN, MACUNIC APPLICANT: WANAHAN, MACUNIC APPLICANT: WANAHAN SANOGHISA APPLICANTON SANOGHISA APPLICANT: WANAHAN SANOGHISA ANAHAN SA

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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sheppard, Faul O.
APPLICANT: Sheppard, Faul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PRC;
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2011-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-226-420-9
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LENGTH: 432
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                                                                                                                                                                                                            CTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC 240
                                                                                                                                                                                                                                                    241 AGTTATGAGAATTGGATTGAAGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GGGITTCATAAGIGGGAGAATTITTACIGIGAACAACAAGAICCTTTTGICIGCGAGGC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAYTAYCAYAARTGGGTNAAYATHTAYTGYGGNGARATHAAYCCNTTYGTNTGYGARGC 455
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NAME/KEY: misc_feature
LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, LOCATION: 66, 69, 78, 81, 84, 90, 93, 114, 117, 129, 135, 147, 153, LOCATION: 162, 171, 17, 180, 186, 189, 192, 201, 204, 213, 216, 222, LOCATION: 225, 231, 234, 237, 246, 249, 252, 255, 261, 276, 279
OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
LOCATION: 282, 285, 291, 309, 312, 321, 327, 330, 333, 336, 339, 360,
LOCATION: 366, 372, 378, 381, 384, 393, 396, 414, 429, 441, 447, 456
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAPPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND
FILE REPRENDENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50 DE NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10226420; Publication No. US20030157686A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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US-10-226-420-6
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Best Local Si
Matches 1699
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NAME/KEY: misc. feature
LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 11
LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 18
LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 27
LOCATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 45.7%; Pred. No. 3.7e-49;
Matches 163; Conservative 85; Mismatches 109; Indels
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301
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NAME/KEY: misc feature
LOCATION: 6, 15, 18, 21, 24, 27, 45, 57, 78, 81, 93, 96, 99, 111, 10CATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180, 10CATION: 285, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276, OTHER INFORMATION: 8, 77, 0.0 315, 327, 330, 345, 348, 360
                                                                                                                                                                                                                                                        OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
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Patent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
TITLE BISHOP, Paul D.
TITLE PERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT APPLICATION NUMBER: US/206,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASELSEQ for Windows Version 4.0
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CAMINE KEST: misc feature

LOCATION: 363, 376, 378, 384, 393, 405, 423,

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                            SEQ ID NO 9
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61 TGCACGAAGCAGGTGAACGGGGGATCTCTGTCTATCGAAAGCTCCGGAGAAGCAGAC 120
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                                FEATURE:

OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:11.

NAME/KEY: misc feature for 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, 100CATION: 66, 69, 84, 87, 90, 99, 120, 123, 132, 135, 141, 153, 159, 10CATION: 168, 177, 183, 186, 195, 196, 285, 288, 303, 315, 318, 10CATION: 337, 240, 243, 246, 273, 282, 285, 288, 303, 315, 318, 37, 10CATION: misc feature in AME/KEY: misc feature in CCATION: 327, 333, 336, 339, 342, 345, 357, 360, 366, 372, 387, 390, 10CATION: 402, 411, 426, 447, 453, 465, 468

COCATION: 0.0 CHER INFORMATION: n = A,T,C or G US-0929-230-12
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LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, 50CATION: 6, 9, 21, 24, 30, 39, 120, 123, 132, 135, 141, 153, 159, LOCATION: 168, 177, 183, 186, 192, 195, 198, 201, 219, 222, 228, 231, DCCATION: 237, 240, 243, 246, 273, 282, 285, 288, 303, 315, 318
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%; Score 166; DB 10; Length 474; 43.4%; Pred. No. 4.8e-46; Live 88; Mismatches 114; Indels
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) Sequence 12, Application US/10226420
) Publication No. US20030157686A1
) GENERAL INKORMATION:
) APPLICANT: Sheppard, Paul O.
) TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
) TILLE REFERENCE: 00-72
CURRENT APPLICANT APPLICATION NUMBER: US/10/226,420
) CURRENT FILING DATE: 2002-08-21
) NUMBER OF SEQ ID NOS: 14
) SOFTWARE: FastUSEQ for Windows Version 4.0
) SEQ ID NO 12

LENGTH: 474
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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           NAME/KEY: misc_feature;
COCATION: 327, 333, 336, 339, 342, 345, 357, 360, 366, 372, 387, 390, 10CATION: 402, 411, 426, 447, 453, 465, 468
COTHER INFORMATION: n = A,T,C or G
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                                                                                                                             Query Match 30.5%; Score 166; DB 13; Length 474; Best Local Similarity 43.4%; Pred. No. 4.8e-46; Matches 155; Conservative 88; Mismatches 114; Indels
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Fatent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT APPLICATION NUMBER: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 220; Conservative
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Zsnk2
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LENGTH: 483
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US-09-929-230-1
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US-09-929-230-1
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                                    207 ITTGTGGGCAAACTGGCCTCCCAAACTTTGAAATTCACTTCCA-----TGTGGATCGGA
                                                                                            181 CTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGGGGATGGCTCCAGCATC
                                                                                                                                                                                        241 AGTTATGAGAATTGGATTGAAGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA
                                                                                                                                       261 CTGAAAGATCTATGGAAAG-----AATGCAAATGGCAGTGGAGCGATGACACTG
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Search completed: December 8, 2003, 13:54:34 Job time: 348 secs

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BM401663 PH012R Sn
BM401662 JL2G06F S
BM401668 JL2H08F S
BM401682 PH012F Sn
                                                                                December 8, 2003, 10:20:33 ; Search time 2261 Seconds (without alignments) 5847.694 Million cell updates/sec
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1 GAAGGCATTGCTACAAGGT.....AITCTGCCTAGCCTGAAAAA 544
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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002 NA

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/tissue types="venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, vector: pGBM112£1; Site 1: ECO
RI, Site 2: Not I: Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM112£+ vector (Promega). ESTS
were generated from random clones and grouped in unique
sequences. The putarive identification of each EST or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 ATCCAAATACTATGTCTGGATCGGACTGAGGATTGAAAACAAAAAACAGCAATGCAGCTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAAATCCTTTCGTGCGAGTTCATACGACCGCGTTAAGATCCGGCTGAGTGAAGTCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 GAAGTGGAGCGATTACTCCAGCGTCAGTTATGAGAACCTGGTTCGAGGAAATGTGAAAA 252
                                                                                  and Ho,P.L. and diversity in the venom glands of insularis through the generation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AGCCAAAATCCATGTCTGGATCGGACTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIGITITICCCCTGGAAAAAAGCAAGGGTTTCGTAAGTGGGTCAATATTGACTGTGTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 GACCTGGACAGATGCAGAGAGCTTCTGCACGAAGCAGGTGAACGGGGGGCCATCTGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AGAGTGGAGGGTGCCTCCAGCATCAGTTATGAGAATTGGATTGAAGAAGAATCCAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cluster was obtained through Blast searches (e-value
          Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                              Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 511 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233.8; DB 12; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                              This EST corresponds to cluster BITL07A (see Reference)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGAAGCAAGCCCCCCCCCCCATCCCCCAACCCTGCCT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGAAGCAAGGAGCCCCCCACCCCTTACCCACCCGCCT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.1e-52;
0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Bothrops insularis"
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                                Viperidae, Crotalinae; Bothrops.

1 (bases 1 to 418)

Unnqueira-de-Azevedo, I.L.M. and Hc
A survey of gene expression and di
the pirviper snake Bothrops insula
expressed sequence tags (ESS)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:8723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.7%;
Matches 305; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                         hoplee@usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13F
                                                                                                                                                                                                                     22347338
                                                                                                                                                                                                                                             12459276
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ORIGIN
                                                                                                                                                                                                                MEDLINE
PUBMED
COMMENT
                                                                                  AUTHORS
TITLE
                                                             REFERENCE
                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                   /tissue type="venome glands"
/tissue type="venome glands"
/clone lib="Snake Bothrops insularis library IL2"
/clone lib="Snake Bothrops insularis library IL2"
/note="Organ: venome glands, vector: pGEMILZE+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechhologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZE+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear EST 01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 TGGTCGNTGAGAACAAACACAGTCGCGAATTGAATGTCTGGATCGGAATGAGGGTTCAAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGCAAINTITAACTGTGAACAACGAATTCCTTTNGTCTGCGAGGTATAGTCTGAAGATG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCTGATTGAAGTCTGGAGAAGCAAGGAAGCCCCCCCACCCCATCCCCCAACCCTGCCTA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCTGAGTGAAGTCTGGAGGAAGGAAGCCCCCCACCC---CTCCCCACCCCGCCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 GCCACAATCTCTGCTATGCACCCTTTGCTCAACGGATGCTCTCTGTAGCTGGATCTGGTG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGCAATCTCTGCTCTGCCCCTTCGCTGAACGGATGCTCTCTGTAGCTGGATCTGGGTT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bothrops insularis (island jararaca)
Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM401662 418 bp mRNA linear EST 01-MAY-2 JL2G06F Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAATGGCGGCCATCTGGTNTCTATCGAAAGCGCCGGAGAAGCAGCCTTTGTGGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 TGAACGGGGGGCATCTGGTCTCTATCGAAAGCTCCGGAGAAGCAGACTTTGTGGGCCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 TGATTGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGGATCGGACTGAGGGCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ACAAAGAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATCAGTTATGAGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 GCAAAGAAAAGCAATGCAGC---TCGTGGAGCGATGGCTCCAGCGTCAGTTATGAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATTGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACAGGGTTTCATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATTAAAGCAGAATTAAAAACATGTATTGGGTTGAAAAAAAGATGCAGGGTTTCGTAAGT
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Email: hoplee@usp.br
This EST corresponds to cluster BITL09A (see Reference)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 302; DB 12; Length 461; Pred. No. 3.2e-71; 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGCIGCICCIGAIGGGCCGGAAG--ICAAIAAAIICIGCCIAGC 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Bothrops insularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 t
                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:8723"
                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
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BM401662.1 GI:20376290
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82.2%;
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                                                  primer: M13R
                                                                                                          .461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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BM401662
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KEYWORDS
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BM401682 618 bp mRNA linear EST 01-MAY-2002 PH012F Snake Bothrops insularis library IL2 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                     336 ACAAGAICCITITGICIGCGAG----GCAIAGICIGAAGAICCAGCIGAITGAAGICIG 390
                                                                                                                               459 AGGAAATCCTTTCGTGTGCAAGTTCATACGACCGCGTTAAGATCCGCTGAGTGAAGTCTG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GAAGGGCGTTCCTACAGGTTCTTCAAAGAAGGGGAAAAACTGGGACGATGCANAGAGGTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Bothrops.

Junqueira 1 to 618)

Survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
GTGTCTTGGGGTGCACATAGAGACAGGGTTTCATAAGTGGGAGAATTTTTTACTGTGAACA
                                         399 GIGITITIGCGCIGGAAAAAGCAAGGGITITCGIAAGIGGGICAAIATIGACIGIGIAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:18723"
/tissue type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hoplee@usp.br
This EST corresponds to cluster BITL09A (see Reference)
Seg primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 205; DB 12; Length 61
Pred. No. 8.3e-45;
0; Mismatches 81; Indels
                                                                                                                                                                                                         519 GAGAANCAAGGAAGCCCCCCCCCCCTTACCCCCCC 555
                                                                                                                                                                           391 GAGAAGCAAAGCACCCCCATCCCCCAACCC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .618
/organism="Bothrops insularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bothrops insularis (island jararaca)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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Best Local Similarity 77.1
Matches 297; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /iisue type="Venore glands"
//lone lib="Stake Bothrops insularis library IL3"
//clone lib="Stake Bothrops insularis library IL3"
//note="Organ: venom glands, Vector: pGEMILZE, is ite 1: Eco RI; Site 2: Not I: Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript plasmid System for CDNA Synthesis and Cloning (LifeTechhologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agazose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZE+ vector (Promega). ESTS were generated from random clones and grouped in unique sequences. The putative identification of each EST or
                                                                EST 01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 TATCGAAAGCGATGAAGAAGCAGACTTTGTGGCCCCAGCTGGTCGCTCCGAACATAGGGAA 278
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                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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                                                                                                                                                                                                                                                                                                                        Jungueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothroops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                       BM401668 Losa 556 bp mRNA linear EST 01-MAY-2
JL2H08F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL07A (see Reference)
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Pred. No. 1.5e-49;
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/db_xref="taxon:8723"
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paul
Tel: 55 11 37 26 7222 ext. 2083
Pax: 55 11 37 26 1505
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/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, vector: pGEMI12E; site 1: Eco
RI; Site 2: Not I; Sug of manA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMI12E; vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
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Junquelra-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
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                      TITGIGGCCCAGITGAITGCTCAGAAGAIAAAGICAGCCAAAAAICCAIGICIGGAICGGA
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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/db_xref="taxon:8723"
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BM401634 11near BST 01-MAY-2002 JLIG02F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                 161 gagcrosrargargcagagarrergeregageaggcagggaaaggeggeggegrerereere
                                                                                                                                                                                                                                                                                                                                                                                           TATCGAAAGCTCCGGAGAAGCAGACTTTGTGGGCCAGTTGATTGCTCAGAAGATAAAGTC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 TATCGAAAGCGATGAAGAAGAACTTTGTGGCCCAGCTGGTCGCTCCGAACATAGGGAA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AGAGTGGAGCGATGGCTCCAGCATCAGTTATGAGAATTGGATTGAAGAAGAATCCAAAAA 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTTTTGCGCTGGAAAAAAAGGCAAGGGTTTCNTAAGTGGGTCAATATTGACTGTGANA 460
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1 (Dases 1 to 370)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                 95
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/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis thouse="Organ: venom glands; Vector: pGEMILZF+; Site 1:
RI, Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse
                                                                                                                                                                                                                                                 GACCTGGACAGATGCAGAGGCTTCTGCACGAAGCAGGTGAACGGGGGGGCATCTGGTCTC
                                                                                                                                                                           Gaps
                                                                                                                                                                           0;
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                                                                                                    12; Length 501;
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This EST corresponds to cluster BITL07A (see Reference)
others
                                                                                                                                                                           Indels
                                                                                                                                                                           80;
                                                                                                Score 203.8; DB 1
Pred. No. 1.7e-44;
0; Mismatches 80
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This EST corresponds to cluster
                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8723"
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Gene 299 (1-2), 279-291 (2002)
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             130 g
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Centro de Biotecnologia
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Best Local Similarity 76.2%;
Matches 227; Conservative
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                             Seq primer: M13F
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TITLE
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BM401460
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                                             FEATURES
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transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILIE+ vector (Promega). ESTs sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM401641 418 Depthrops insularis library linear EST 01-MAY-2002 JLH06F Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothroops insularis through the generation of
expressed sequence tags (ESTS)
Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                              Score 195.6; DB 12; Length 370;
Pred. No. 2.6e-42;
0; Mismatches 78; Indels 9;
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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76.2%;
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92 c
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Best Local Similarity 76.23
Matches 279; Conservative
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                                                                                                                                                                       BASE COUNT
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ORGANISM
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AUTHORS
TITLE
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MEDLINE
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KEYWORDS
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/tissue type="venong glands"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis;
/note="Organ: venom glands, Vector: pGEMIJZF; Site 1: Eco
RI, Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMIJZF+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
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JH1D06F Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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BITL07A (see Reference)
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Pred. No. 6.7e-40;
0; Mismatches 71; Indels
                                                                                                                                    organism="Bothrops insularis"
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Bothrops insularis (island jararaca)
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us-09-938-114-1.rst

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149
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BM401418.1 GI:20376046
                                     Centro de Biotecnologia
Instituto Butantan
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Best Local
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ORIGIN
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TITLE
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  PUBMED
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                                                                                                                                                                                                                 /tissue type="webow glands"
/close lib="Snake Bothrops insularis library IL3"
/close lib="Snake Bothrops insularis library IL3"
/note="Corgan: venom glands vector: pGEMILIZ+; Site_1: Eco
RI, Site_2: Not I, Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMILIZ+ vector (Promega). ESTs
were generated from random clones and grouped in unique
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1 (bases 1 to 511)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tagg (BZTS)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05) "
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Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900 Tel: 55 11 37 26 7222 ext. 2083 Fax: 55 11 37 26 1505 Email: hople@ugp.br This BST corresponds to cluster BITL13A (see Reference)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 186; DB 12; Length 460;
Pred. No. 1.1e-39;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 TGTTATGAGAACCTGGTTGAACGAAGAACGAAAAAATGTTTTGTGTTGGA
                                                                                                                                                             /organism="Bothrops insularis"
/mol_type="mRNA"
/db xref="taxon:8723"
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                                                                                                                         Location/Qualifiers
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al Similarity 77.6%;
225; Conservative
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                                                                                                      Seq primer: M13F
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Best Local
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DEFINITION
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MEDLINE
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TITLE
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/Lisue type="Venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, vector: pGEMIJZE+; Site_1: Eco RI; Site_2: Not I: Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZF+ vector (Promega). ESTE were generated from random clones and grouped in unique sequences. The putarive identification of each EST or cluster was obtained through Blast searches (e-value <
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1 (bases 1 to 657)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
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Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900 Tel: 55 11 37 26 7222 ext. 2083 Fax: 55 11 37 26 1505 Email: hoplee@usp.br
This BST corresponds to cluster BITL07A (see Reference) Seq primer: M13F.
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/organism="Bothrops insularis"
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Bothrops insularis
                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:8723"
                                                                                                                                                                                                                             location/Qualifiers
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121 TITGTGGGCCAGTTGATTGCTCAGAAGATAAAGTCAGCCAAAATCCATGTCTGGATCGGA 180
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/organism="Bothrops insularis"
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Contact: Paulo Lee Ho
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Best Local Similarity 79.9%;
Matches 203; Conservative (
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TITLE
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL2"
/clone lib="Snake Bothrops insularis library IL2"
/clone lib="Snake Bothrops insularis library IL2"
/note="Organ: venom glands, Vercor: pGEMIL2F; site l: Eco RI; Site 2: Not I: Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZF+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 GAGCGATGTCTGGAAAG-----GATGCAGGTTCGAGTGGAGCGATGGCAGGGACCTCAG 300
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the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGGTTCTG
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                                                                                                                                                                           Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 722 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL10A (see Reference)
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0; Mismatches 167; Indels
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/db_xref="taxon:8723"
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Contact: Paulo Lee Ho
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/mol type="memory"
//mol type="memory"
//mol type="memory"
//db_xref="taxon:8723"
//tiskue type="venom glands"
//clone lib="Snake Bothrops insularis library IL3"
//clone lib="Snake Bothrops; Vector: pGEM12f+; Site 1: Eco
//clone lib="Snake Bothrops insularis
//note="Organ: venom glands; Vector: pGEM12f+; Site 1: Eco
//note="Organ: venom glands; Vector: pGEM12f+; Site 1: Eco
//note="Organ: venom glands were primed with Oigo-dfT) and reverse
ranscribed to cDNA Superacript Plasmid System for
CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco IR adapters and
directionally cloned in pGEM12f+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
//cone. EST 01-MAY-2002 215 275 Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Lepidosauria; Squamata; Scleroglossa, Serpentes; Colubroidea; Viperidea; Crotalinae; Bothrops.

1 (bases 1 to 406)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS) 62 IGTAGCTGGATCTGGTTTTGCTGCTCCTGATGGGCCAGAAGGTCCAATAAATTCTGCCTA 3 09 BM401598 406 bp mRNA linear EST 01-MAY-2 JH4FllF Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence. cluster was obtained through Blast searches (e-value < 61 TGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTTATCGAAAGCTCCGGAGAAGCAGAC 156 GAAGGGGTTCCTACAGGTTCTTCAAAACACCGAAAAACTGGGGACGATGCAGAGAGGTTC 1 GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAGAGCTTC Gaps Centro de Biotecnologia Instituto Butantan Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900 Fax: 55 11 37 26 7222 ext. 2083 3; Email: hoplee@usp.br This EST corresponds to cluster BITL15A (see Reference) Score 161.2; DB 12; Length 406; Pred. No. 5.9e-33; 0; Mismatches 48; Indels 3; .9e-33; es 48; Indels

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36 GACCTGGACAGATGCAGAGAGCTTCTGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTC
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Pred. No. 1.4e-31;
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/db_xref="taxon:8723"
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Best Local Similarity 77.7%;
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hoplee@usp.br
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//Listue type="venom glands"
//Lone lib="Snake Bothrops insularis library II3"
//Lone lib="Snake Bothrops insularis library II3"
//Lone lib="Snake Bothrops insularis library II3"
//Lone Bothrops insularis
//Lone Bothrops insularis
//Lone library II3 and reverse
//Lone transcribed to cDNA using Superscript Plasmid System for
CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
//Lone selected by size (350-600 pb and up 600 pb) in
//Lone selected by size (350-600 pb and up 600 pb) in
//Lone selected from random clones and grouped in unique
//Lone sequences. The putarive identification of each EST or
//Luster was obtained through Blast searches (e-value 
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                                                                                                                                                                                                                                                                                            JAHO7F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence. BM401605
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        CTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGCGATGGCTCCAGCATC 240
                                                                                                  336 ATGAAGGTTCAAGGCAAAGAAAAGCAATGCAGC---TCGTGGAGGGATGGCTCCAGCGTC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

Ju (bases 1 to 410)

Junqueira-de-Azevedo, L.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
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0
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Centro de Biotecnologia
Instituto Butantean
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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Seg primer: M13F.
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'db_xref="taxon:8723"
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Best Local Similarity 78.0%;
Matches 192; Conservative
                                                                                                                                                          241 AGTIATGAGAATIG 254
                                                                                                                                                                                                393 AGTTATGAGAACTG 406
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/tisque type="venom glands"
/clone lib="Snake Bothrops insularis library IL13"
/clone lib="Snake Bothrops insularis library IL13"
/clone lib="Snake Bothrops insularis library IL13"
/clone lib="Snake Bothrops insularis librared" or I so to the library library IL13"
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGENLIZf, vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < 0 BM401653 453 bp mRNA linear EST 01-MAY-2002 JL2D01F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence. 341 gaagiggagcgainachccagcgrcagthardagaaccrgghcgaggaaangrgaaaa 400 Eukaryota; Metazas, Chordata, Craniata; Vertebrata, Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 453)

Junqueira-de-Azevedo,I.L.M. and Ho,P.L.

A survey of gene expression and diversity in the venom glands of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002) 156 AGCCAAAATCCATGTCTGGATCGGACTGAGGGCTCAAAAACAAAGAAAAGCAATGCAGCAT 281 Arccadaracraticricidiaricidadicridadariticada a Arccada a Arcc 216 AGAGTGGAGCGATGCTCCAGCATCAGTTATGAGAATTGGATTGAAGAAGAATCCAAAAA Gaps ö Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505 Length 453; This EST corresponds to cluster BITL07A (see Reference) 54; Indels

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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM401659
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BM401659
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/tissue_type="wenom glands"
/tissue_type="wenom glands"
/clone_lib="wenom glands; wector: pGEM11Zf+; Site_1:
/note="Organ: wenom glands; wector: pGEM11Zf+; Site_1: Site_2: Not I; Sug of mRNA from Bothrops insularis wenom glands were primed with oligo-(dT) and reverse venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco_RI adapters and
                                                                                                                                                                                                                                                                                                                                                                                                                 BM401459
JH1D05F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
96 TAICGAAAGCICCGGAGAAGCAGACTITGIGGGCCAGITGAITGCICAGAAGAIAAAGIC 155
                                                                                         272 TATCGAAAGCGAIGAAGAAGCAGACTTTGTGGCCCCAGCTGGTCGCTCCNAACATAGGGAA 331
                                                                                                                                156 AGCCAAAATCCATGTCTGGATCGGACTGAGGGCTCAAAACAAAGAAAAGCAATGCAGCAT 215
                                                                                                                                                           216 AGAGTGGAGCGATGGCTCCAGCATCAGTTATGAGAATTGGATTGAAGAAGAATCCAAAAA 275
                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jungueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothroops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
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This EST corresponds to cluster BITL07A (see Reference)
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Centro de Biotecnologia
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/Lissue type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lorgan: venom glands; vector: pGEM11Zf+; Site_1: Eco
/note="Organ: venom glands; vector: pGEM12Zf+; Site_1: Eco
/note="Organ: venom glands; vector: pGEM1Zf+; Site_1: Eco
/note="Organ: venom glands insularis
/comparison of mena from Bothrops insularis
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Viperidae, Crotalinae, Bothrops.

Junqueira-de-Azevedo, L.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL07A (see Reference)
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Pred. No. 1.7e-30;
0; Mismatches 48;
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/mol_type="mRNA"
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Bothrops insularis
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                                            36 GACCTGGACAGATGCAGAGGCTTCTGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTC 95
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Matches 180; Conservative. 0; Mismatches 51; Indels
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Search completed: December 8, 2003, 12:39:48 Job time : 2262 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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sw model using protein search, OM protein

8, 2003, 09:45:44; Search time 77.4 Seconds (without alignments) 264.544 Million cell updates/sec December Run on:

US-09-938-114-2 Title: Perfect score:

Scoring table: Sequence:

1107863 seqs, 158726573 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

A Geneseq 197un03:*

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| SIDSI/gcgdata/geneseqp_embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf_emeseqp_embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqg_emeseqp_embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqg_emeseqp_embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseqg_emeseqp_embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseqg_emeseqp_embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqg_emeseqp_embl/AA1989.DAT:*
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| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqg/genese /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.bA::* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAF:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Deinagkistrodon ac	Pigmy rattlesnake	Snake venom blood Korean adder snake	Pigmy rattlesnake	Sequence of polype	Botrocetin alpha s	Ahylysantinfarctas	Sequence of polype
ΩÏ	4 ABU08798	3 AAE20179	AAM51543 AAO14520	3 AAE20180	4 AAR38222	1 AAR45156	3 ABB79130	4 AAR38226
% Query e Match Length DB ID	129 24	152	154 2	144 23	131 1/	133 14	132 2	132 14
% Query Match L	100.0	7.90	64.3	60.7	59.3	59.1	57.4	56.8
Score	715	4//	460	434	424	422.5	410.5	406
Result No.	н с	7 C	O 4	rV.	9	7	00	σı

·	Ö	se of	ttle	Vipera palestinae	Segmence of polype	ō	A	Snake venom blood	4 Y63A	K61A	M13-G4 R66A mutant	⋖.	M17-G4 R103A mutan	M20-G4 F108A mutan	Д	Snake venom derive	venom	126-mer wild-type	Snake venom antith	Snake venom derive	149-mer wild-type	M21-G4 D54A, D101N		M18-G4 R105A mutar	M19-G4 E106A mutar	M23-G4 D54N, D101A	M24-G4 D54A, D101F	M16-G4 D101A mutar	M25-G4 D101A, E106			M26-G4 D101A, E106	₩	Sequence of the pl	Worker adder chale
	AAK38223	AAR38228	AAE20181	AAR72235	AAR38230	AAR38225	AA020982	AAM51544	AA020985	AA020983	AA020986	AA020988	AA020990	AA020993	AA020981	AAR71979	AAY85627	AA020973	AAR71981	AAY85628	AA020974	AA020994	AA020984	AA020991	AA020992	AA020996	AA020997	AA020989	AA020998	AA020987	AA020995	AA020999	AA020980	AAR24426	LC27 LOEE
,	14	14	23	16	14	14	23	22	23	23	23	23	23	23	23	16	21	23	16	21	23	23	23	23	23	23	23	23	23	23	23	23	23	13	23
		130	158	132	133	123	126	146	126	126	126	126	126	126	126	126	126	126	149	149	149	126	N	N	N	3	$^{\circ}$	126	126	126	2	126	126	127	140
		'n.	54.1	ά.	43.2	41.0	40.9	40.6	40.5	•	40.3	40.3	40.3	40.3	40.2	40.1	40.1	40.1	40.1	40.1		39.9	φ.	ď.	9.	9.	ę.	9.	39.7	ę.	9.	6			20
	*	395	387	372	309	293	292.5	290	289.5	288.5	288.5	288.5	288.5	288.5	287.5	286.5				286.5		285.5							283.5					4.	272 E
	1	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44

ALIGNMENTS

ABU08798 standard; Protein; 129 AA (first entry) 02-JUN-2003 ABU08798; RESULT 1 ABU08798

Deinagkistrodon acutus antithrombosis enzyme alpha chain.

Antithrombosis, alpha chain; fibrin hydrolysis; blood clot; enzyme; platelet aggregation; vaso-occulusive disorder; thromboembolic disorder; myocardial infarction; restenosis; cancer; neurodegenerative disease; angiopathic thrombosis; cerebral thrombosis; thrombosis; obliterans; ischaemic cerebral vascular disease, unstable angina; acute thrombosis; unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema; peripheral arterial occulsion; stroke; atherosclerosis; inflammation; thrombosis

Deinagkistrodon acutus.

Location/Qualifiers Region

/note= "Antithrombosis enzyme alpha chain N-terminus not encoded by abx93668" /note= "Specifically claimed in claim 7" 91Misc-difference Region

/note= "Encoded by TAT"

US6489451-B1

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The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis was administered to rabbits intravenusly. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the cloudler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.050 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thrombosition is useful for preventing and treating vaso-occulusive and thrombosition chrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thrombosiitis obliterans, pulmonary embolism, deep vein thrombosis, peripheral arterial occulsion, stroke. It is also useful for treating attentiosclarosis, occume and inflammation, cancer and neurodegenerative diseases. The present sequence represents the amino acid sequence of the perinagkistrodon acutus antithrombosis enzyme alpha chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                   New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and unstable angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; Zsnk3.
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Pred. No. 2.8e-68;
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                                                                                                          (HEFE-) HEFEI SIU FUNG USTC PHARM CO LID.
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                                                                                                                                                                                                                                                                                                                            Claim 12; Column 11; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE20179 standard; Protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Sc
100.0%; Pr
tive 0;
                                  98US-0058740
                                                                      97US-043886P
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                                                                                                                                                                                WPI; 2003-352116/33.
N-PSDB; ABX93668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AA;
                                                                                                                                              Cheng X;
                                   LO-APR-1998;
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system. The polypeptides, which affect blood coagulation and platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory protein chemistry and antibody production and analysis. The polypeptide can be used as standards or as unknowns polymucleotide or polypeptide can be used as standards or as unknowns to testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tagin, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 RALLYIWIGLRVQGKEKQCSAKWSDGSSVSYENWIEAESKTCLGLQQGTNYHKWVNIYCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                               New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
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; Pred. No. 7.8e-43;
16; Mismatches 30;
1..23
/label= Signal_peptide
24..152
/label= Mature_Zsnk3_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM51543 standard; Protein; 152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.78;
                                                                                                                                                                                                                                               2000US-225087P.
2000US-225489P.
2000US-225490P.
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53..150
125..142
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EINPFVCEA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecular biology
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                                                          Disulfide-bond
Disulfide-bond
                                                                               Disulfide-bond
Disulfide-bond
                                                                                                                                 WO200214364-A2
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20-DEC-2000;
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15-AUG-2000;
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                                Protein
 Peptide
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 DCPSGWSSYEGHCYNIFHLFKTWAEAERFCRKQVKGAHLVSIESSEEADFVAQLVSENMK
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence is the A chain of halyxin.
                                                                                                                                                                                                                                                                                                                                  Halyxin as blood anticoagulation protein separated from snake venom
                                                                            Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Korean adder; salmorin protein A chain; snake venom;
fibrinogen clotting inhibition; thrombosis; prothrombin binding;
thrombin binding; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.4%; Score 475; DB 22; Length 152; 63.6%; Pred. No. 1.3e-42; ative 17; Mismatches 30; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korean adder snake venom salmorin A chain protein.
                                                          Snake venom blood anticoagulant halyxin A chain.
                                                                                                                                                                                                                                                                            Son
                                                                                                                                                                                                                                                                           BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                           Koo
                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 10; 21pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agkistrodon halys brevicaudus
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                                                                                                                                                                                               29-JUN-2000; 2000KR-0036591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                         Jung GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::||||||
144 ERNPFVCEA
                                                                                                                       Agkistrodon halys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAI71876
                                                                                                                                              KR2001049671-A
                                                                                                                                                                                                                        29-JUN-1999;
                                   10-JAN-2002
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                                                                                                                                                                        15-JUN-2001
           AAM51543;
                                                                                                                                                                                                                                                                        Jang YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA014520;
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The invention comprises the nucleotide and protein sequences of a salmorin protein derived from the venom of Korean adder. Salmorin protein is composed of an A chain and a B chain, and has inhibitory activity against fibrinogen clotting. The salmorin protein of the invention is useful for treating thrombosis, as it represses fibrinogen clotting potently by binding to prothrombin and thrombin so as to delay blood coagulation. The present amino acid sequence represents the Korean adder salmorin A chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEEŞKKCLGVHIETGFHKWENFYCEQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 CPSGWGSNNGHCYQAFNQRMTWEDABRFCSAQAKGGHLVSIETRABADFVAHVVABRRIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                  New salmorin protein derived from venom of Korean adder Agkistrodon halys brevicaudus, useful for treating thrombosis by repressing fibrinogen clotting through repression of activation of prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pigmy rattlesnake, venom gland protein; blood coagulation; therapy; platelet aggregation; Zsnk4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 154;
                                       /note= "Mature salmorin A chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.3%; Score 460; DB 23;
60.2%; Pred. No. 5.1e-41;
live 20; Mismatches 31;
 1..23
/label= Signal_peptide
24..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pigmy rattlesnake venom gland protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE20180 standard; Protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1A; 30pp; English.
                                                                                                                    26-JUL-2001; 2001WO-KR01277.
                                                                                                                                              27-JUL-2000; 2000KR-0043470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                         (BIOB-) BIOBUD CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 QDPFVCEA 129
                                                                                                                                                                                                                            WPI; 2002-241907/29.
N-PSDB; AAL42015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::||||||
147 RNPFVCEA
                                                                                                                                                                                                     Chung K, Kim D,
                                                                WO200214514-A1
                                                                                                                                                                                                                                                                                                              into thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-2002
                                                                                          21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE20180;
Peptide
                           Protein
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AAE20180
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Protein

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SAKIHVWIGLRAQNKEKOCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DCPSDWSSYDQYCYRVFKRLQTWEDAERFCSQQANDGHLVSIESAGEADFVTQLVSENIR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 kDa and about 15 kDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of AAR38224 has been found, characterised by Asp at posn. three in lieu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botrocetin; alpha subunit; snake venom; Bothrops jararaca; von Willebrand factor; von Willebrand disease.
                                                                           polypeptide chain of alboaggregin A (AL-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.3%; Score 424; DB 14;
57.0%; Pred. No. 2.8e-37;
ive 22; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                    Venom; snake; platelet-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR45156 standard, protein; 133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 45; 74pp; English
                                                                                                                                                                                                                                                                                   92WO-US10344.
                                                                                                                                                                                                                                                                                                                            91US-0803630.
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                 (updated)
(first entry)
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nes 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botrocetin alpha subunit.
                                                                                                                                                           Trimeresurus albolabris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-196991/24.
                                                                                                                                                                                                                                                                                                                                                                                      (UTEM ) UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                                                                               Kirby EP, Peng M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AA;
                                                                                                                                                                                                                                                                                   01-DEC-1992;
                                                                                                                                                                                                                                                                                                                            03-DEC-1991;
                                                                                                                                                                                                    WO9311151-A1
                                                                                                                                                                                                                                                                                                                                                  05-JUN-1992;
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08-JUN-1994
                 25-MAR-2003
01-0CT-1993
                                                                             Sequence of
                                                                                                                                                                                                                                             10-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
practical kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
porties blotting, protein purification, determining the
weight of expressed polypeptides as ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein, Zenk4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 QNKYDVWIGLRIQGEEKQCSTKWSDGSSVNYENLIKHATKKCFGLKKETGFRIWRNVHCT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, affect blood coagulation and platelet aggregation system, useful itherapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
                 /label= Mature_Zsnk4_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%; Pred. No. 2.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR38222 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 3; 79pp; English
                                                                                                                                                                                                                                                            14-AUG-2000; 2000US-225687P.
15-AUG-2000; 2000US-225489P.
15-AUG-2000; 2000US-225490P.
20-DEC-2000; 2000US-356997P.
                                                                                                                                                                                                      13-AUG-2001; 2001WO-US25310.
                                    13..24
41..138
113..130
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                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                              Б,
10..144
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                                                                                                                                                                                                                                                                                                                                                                                                              Sheppard PO, Bishop
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N-PSDB; AAD32057.
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Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecular biology
                                                                           Digulfide-bond
                                    Disulfide-bond
                                                            Disulfide-bond
                                                                                                                      WO200214364-A2
                                                                                                                                                                                                                                             14-AUG-2000;
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Gaps

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33;

Sequence

Query Match

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AAR38222;

RESULT 6 AAR38222

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Length 131;

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Claim 6; Page 47; 74pp; English.
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92US-0893929
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(first entry)
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trimeresurus albolabris
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120 QLNPFVCK 127
                                                                                                                                                                                                                                                                                                     121 QQDPFVCE 128
                                                                                                                                                                                                 Similarity
                        WPI; 2002-281832/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-196991/24.
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                                                                                                                                                                       132 AA;
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Best Local Simi
Matches 75;
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05-JUN-1992;
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01-OCT-1993
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                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                      AAR38226;
     Xiao C;
     임
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                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                        1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIE-SSGEADFVGQLIAQKI
                                                                                                                                                                                                                                                                                                                                    Botrocetin, isolated from Bothrops jararaca venom, is a disulfide-
linked heterodimer comprising an alpha subunit (AAR45156) and a beta
subunit (AAR45157). The protein is used to assay von Willebrand
factor in serum or plasma, for diagnosis of von Willebrand disease.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                       Use of purified botrocetin and opt. ristocetin - for detection of von Willebrand Factor in serum or plasma, for diagnosis of von
                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                      59.1%; Score 422.5; DB 14; Length 133; 56.9%; Pred. No. 4.2e-37; ive 20; Mismatches 35; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ahylysantinfarctase thrombase I; Chinese Agkistrodon acutus; snake venom; enzyme; Deinagkistrodon acutus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ahylysantinfarctase thrombase I subunit A SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB79130 standard; protein; 132 AA.
                                                                                                                                                                                           Disclosure; Page 8; 14pp; English.
                                                      92EP-0305046
                                                                        92EP-0305046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-2001; 2001CN-0115567
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                                                                                                  UNIV FUJITA HEALTH
                                                                                                                                                                                                                                                                                              Local Similarity 56.99
nes 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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| 121 AQKNPFVCKS 130
                                                                                                                                                                                                                                                                                                                                                                                                  120 EQODPFVCEA 129
                                                                                                                    Fujimura Y, Titani K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deinagkistrodon acutus
                                                                                         (GENZ ) GENZYME CORP
                                                                                                                                                                          Willebrand's disease
                                                                                                                                     WPI; 1993-407054/51.
Bothrops jararaca
                                                                                                                                                                                                                                                                     133 AA
                                                     02-JUN-1992;
                                                                        02-JUN-1992;
                  EP574621-A1
                                    22-DEC-1993
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents subunit A of the abylysantinfarctase thrombase I isolated from the snake venom of Chinese Agkistrodon acutus (Deinagkistrodon acutus). The present invention describes an anionic exchange column chromatographic process used to separate and purify, and the repurifying in a fast protein purifying work station, where snake venom of Chinese Agkistrodon acutus. The test shows that the Ahylysantinfarctase thrombase I consists of two subunits designated and a lee ABB79130 and ABB79131 respectively).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 132;
Ahylysantinfarctase thrombase and its production process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 410.5; DB 23; Length
58.6%; Pred. No. 7.9e-36;
tive 18; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of polypeptide chain of alboaggregin B1 (AL-B1).
                                                                        Claim 4; Page 5 (Disclosure); 8pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venom; snake; platelet-binding protein.
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us-09-938-114-2.rag

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Sequence
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                                                                                                                                                                                                                                                                                   61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIREESKKCLGVHIRTGFHKWENFYCE 120
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                                                                                                                                                                                                                             1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                                                                                                                                                AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 KDa and about 15 KDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of AAR38224 has been found, characterised by Asp at posn. three in lieu
                                                                                                                                                                                                  Gaps
Alboaggregin B1 and B2 (collectively "AL-B"), may be obtained in substantially pure chemical form from venom. Each of AL-B11 and -B2 comprise an about 23 kDa protein formed by an about 17 kDa polypeptide chain crosslinked to an about 14 kDa polypeptide chain crosslinked to an about 18 kDa polypeptide chain by one or more interchain disulfide bonds. Each of the two polypeptide chains of AL-B1 and -B2 show strong homology to two of the chains of AL-B1 and -B2 each comprise two non-identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
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                                                                                                                                                                      Length 132;
                                                                                                                                                                                                    35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of polypeptide chain of alboaggregin A (AL-A).
                                                                                                                                                                        56.8%; Score 406; DB 14; 54.7%; Pred. No. 2.4e-35; ive 23; Mismatches 35;
                                                                                                    polypeptide chains. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snake; platelet-binding protein.
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(first entry)
                                                                                                                                                                                     Local Similarity 54.7
hes 70; Conservative
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121 QKHIFMCK 128
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                                                                                                                                               132 AA
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01-OCT-1993
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(Updated on 25-MAR-2003 to correct PN field.)

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                                                                                                                                         62 AKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEBEBSKKCLGVHIETGFHKWENFYCEQ
                                                                                  2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS
                                                                                                      4 CLPGWSAYDQYCYRVFNEPRNWEDAERFCARQADSGHLVSIETMGEADFVAQLISENIQS
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alboaggregin B1 and B2 (collectively "AL-B"), may be obtained in substantially pure chemical form from venom. Bach of AL-B11 and -B2 comprise an about 17 kDa protein formed by an about 17 kDa polypeptide chain crosslinked to an about 14 kDa polypeptide chain crosslinked to an about 14 kDa polypeptide chain py one or more interchain disulfide bonds. Each of the two polypeptide chains of AL-B1 and -B2 show strong homology to two of the chains of AL-A. AL-B1 and -B2 each comprise two non-identical polypeptide chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
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                      Length 134;
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                                                     34; Indels
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Pred. No. 3.5e-34;
                         ; Score 404; DB 14;
; Pred. No. 3.9e-35;
22; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Venom; snake; platelet-binding protein.
                                                                                                                                                                                                                                                                                                         AAR38228 standard; protein; 130 AA.
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                           56.5%;
55.9%;
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92US-0893929.
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Best Local Similarity 54...
Best Tocal Similarity
Tocal Conservative
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(first entry)
                                                        Conservative
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134 AA
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05-JUN-1992;
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                                Ma.
Local Sim.
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01-OCT-1993
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36; Indels

Length 158;

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identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland protein, Zsnk5.
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                                                                                                                                                                                      54.1%; Score 387; DB 23; 52.3%; Pred. No. 3.1e-33; live 25; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 19; 37pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0002691.
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67; Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 QQDPFVCE 128
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                                                                                                                                              158 AA;
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04-DEC-1995
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                                                                                                                                                Sequence
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Matches
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                                                                                             --KYHVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPNPKKCFVLKKESEFKTWSNVYCE 118
                                                                  SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system. The polypeptides, which affect blood coagulation and platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory practical kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The polymucleotide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; Zsnk5.
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/label= Signal_peptide
24..158
/label= Mature_Zsnk5_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pigmy rattlesnake venom gland protein, Zsnk5.
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2000US-225489P.
2000US-225490P.
2000US-356997P.
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QKHIFMCK 126
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15-AUG-2000;
15-AUG-2000;
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145
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           82
86 QNQYYWIGLRIQNKGQQCSTKWSDGSSVSYENLVKSHSKKCFGLKKETEFLQWYNTDCE
                              61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR72235 is a Vipera palestinae venom derived peptide. A peptide compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti-thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 132;
                                                                                                                                                                                                                                                        Vipera palestinae, venom, antithrombotic agent, platelet binding, von Willebrand factor.
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Pred. No. 9.9e-32;
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                                                                                                                                                                                                                                  Vipera palestinae venom derived peptide.
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49.6%;
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119 CEQQDPFVCEA 129

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RESULT 15
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                  1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                    63 KSKYHAMIGLRDQSERQQCSSHWTDGSAVSYET--VTKYTKCFGLNKDKGYLEWVTLPCB
                                 3 DCPSDWSSHEGHCYKVFRLFKTWBEAEKFCMQQVNGWHLASIESVBEANFVAELVSKTLI
                                                          SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                          Sequence of polypeptide chain of alboaggregin-like protein called
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43.2%; Score 309; DB 14; Length 133;
Best Local Similarity 47.3%; Pred. No. 5.1e-25;
Matches 62; Conservative 24; Mismatches 39; Indels
 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Updated on 25-MAR-2003 to correct PN field.)
  27; Mismatches
                                                                                                                                                                                                                                                                         Venom; snake; platelet-binding protein.
                                                                                                                                                                       AAR38230 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 49; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                        92WO-US10344
                                                                                                                                                                                                                                                                                                                                                                           91US-0803630
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(first entry)
  64; Conservative
                                                                                                    QQDPFVCEA 129
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                                                                                                                                                                                                                                                                                             Echis carinatus.
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01-OCT-1993
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
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46.9%; Pred. No. 2.4e-23;
iive 18; Mismatches 42;
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Job time : 78.4 secs
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                                                                                                                                AAR38225 standard; protein; 123 AA.
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92US-0893929.
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(first entry)
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119 CEFKFPFVCKA 129
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05-JUN-1992;
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01-OCT-1993
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION NUMBER: «Unknown»
APPLICATION NUMBER: «Unknown»
ATTORNEY/AGENT INFORMATION:
RAME: Chen, Anthony C.
REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1999-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS.
                                                                                          December 8, 2003, 09:50:40; Search time 28.0114 Seconds (without alignments) 194.853 Million cell updates/sec
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                                                                                                                                                       US-09-938-114-2
715
1 DCSSDWSSYEGHCYKVFKQS.....GFHKWENFYCEQODPFVCEA 129
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Sequence 2, 1
Sequence 2, 1
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Sequence 3,
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Sequence 6,
Sequence 10
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Sequence 5
Sequence 2
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Sequence 7
Sequence 7
Sequence 9
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-612-840A-2
US-08-612-840A-8
US-07-614-443A-1
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US-07-614-443A-2
US-08-294-859-2
US-08-481-676-2
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PCT-US92-10344-5
US-07-893-929A-2
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US-07-893-929A-4
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Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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No.
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storage

LENGTH: 129 amino acids TYPE: amino acid

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Sequence Seq	THE SNAKE
US-07-614-443A-5 US-08-294-859-5 US-08-481-676-5 US-07-893-223A-8 US-07-893-223A-8 US-08-840-062-4 US-08-840-062-2 US-08-729-103-4 US-08-729-103-4 US-08-729-103-4 US-08-729-103-4 US-08-729-103-4 US-08-822-261-4 US-08-822-261-4 US-08-822-261-4 US-08-822-652-4 US-08-464-657-2 US-08-401-530A-4 US-08-401-530A-4	LIGNMENTS in XY Li, Xin Cheng, Niu, Wan-Zhi Huang, uo, Lian-Di Kang, g Rong, Yan Liu and HROMBOSIS ENZYME FROM AGKISTRODON ACUTUS Street tte, 1.44 Mb
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50 128 1479 1479 16479 16479 1747 1747 1747 1747 1747 1747 1747 1	Application US/0905874(48945). CANT: Chun Wang, Banjan CANT: Chun Wang, Li-Wen Zhen-Yu Xu, Dan IJin-Guo Ding, Far Hui-Ran Chen OF INVENTION: AN ANTITOR ROF SEQUENCES: 12 SPONDERS: 12 SPONDERS: 12 SUDDESSEE: Lyon & Lyon STREET: 633 West Fifth Suite 4700 CITY: LOS Angeles STATE: California COUMTRY: U.S.A. STATE: California COUMTRY: U.S.A. SID: 90071-2066 TER READABLE FORM: MEDIUM TYPE: 3.5" Diske
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27 27 26 26 26 26 26 26 26 26 26 26 26 26 26	RESULT 1 US-09-058-740; Sequence 2, Patent No. GENERAL 1 CENERAL 1 TITL TITL NUMB CORR

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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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0
                                        100.0%; Score 715; DB 4; Length 129; 100.0%; Pred. No. 7.1e-71; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/07893929A
Patent No. 533667
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
MUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.4%; Score 425; DB 1, 57.0%; Pred. No. 4e-39;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NAME: US/07/893,929A
FILING DATE: 19920605
CLASSTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONBACO, Daniel A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFRENCE/DOCKET NUMBER: 6056.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEX: No. 2336676
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
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                                      Query Match
Best Local Similarity 100.
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                         121 QQDPFVCEA 129
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-07-893-929A-1
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  US-09-058-740-2
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 406 University Services Building CITY: Philadelphia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRI: 21P: 19122
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 720 morth RR: IBM PS/2 MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILLING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                              PCT-US92-10344-1

Sequence 1, Application PC/TUS9210344

GENERAL INFORMATION:

APPLICANT: Riby, Edward P.

APPLICANT: Peng, Man-ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 131 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (215) 568-5549
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Matches 73; Conservative
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OPERATING SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US92-10344-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.8%; Score 406; DB 1; Length 132; 54.7%; Pred. No. 4.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
PCT-US92-10344-5
; Sequence 5, Application PC/TUS9210344
; GENERAL INFORMATION:
    APPLICANT: Rirby, Edward P.
    APPLICANT: Peng, Man-ling
    TITLE OF INVENTION: Alboaggregins: Platelet
    TITLE OF INVENTION: Agonists Which Bind To Platelet
    TITLE OF INVENTION: Membrane Glycoprotein Ib
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
                                                        APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education STREET: 406 University Services Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple University - Of The Common-
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FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
Sequence 5, Application US/07893929A
Patent No. 5336667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 605
TELECOMMUNICATION: TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (215) 568-5549
TELEK: NO. 5336667e
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 132 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                           ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: N
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                                    GENERAL INFORMATION:
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61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEBESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DCPSDWSSFKQYCYQIVKELKTWEDAEKFCSEQANDGHLVSIESYREAVFVAELLSENVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.8%; Score 406; DB 5; Length 132; 54.7%; Pred. No. 4.8e-37; Live 23; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07893929A
Patent No. 533667
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION Alboaggregins: Platelet
TITLE OF INVENTION Alboaggregins: Platelet
TITLE OF INVENTION Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: Wealth System of Higher Education
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    # wealth System of Higher Education
for University Services Building
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION UNDERER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INPORMATION:
NAME: MOAGO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECHOME: (215) 568-8383
TELEFAX: (215) 568-8383
406 University Services Building
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KD
COMPUTER: TBM FS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
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MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 132 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.7%
.......ss 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: None INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                               STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
                                           Philadelphia
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121 QKHIFMCK 128
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Gaps

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64 KEHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLGCIQ 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETWGBADFVAQLISENIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Indels
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Patent No. 533667
Patent No. 533667

REDERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Kerg, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF SEQUENCES: 10
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education STREET: 406 University Services Building CITY: Philadelphia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 56.5%; Score 404; DB 5; Best Local Similarity 55.9%; Pred. No. 8.1e-37; Matches 71; Conservative 22; Mismatches 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6056-126 (CIP) 1
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MEDIUM TYPE: Diskette, 3.50 inch, 720 KD COMPUTER: IBM PS/2 COMPUTER: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/893,929A FILING DATE: 19920605 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: AS FILING DATE: December 3, 1991 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                      TELECOMMUNICATION INFORMATION TELEPHONE: (215) 568-8383 TELEFRAX: (215) 568-5549
REFERENCE/DOCKET NUMBER:
                                                                                                                            TELEX: None
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 130 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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TELEX: No. 5336667e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-07-893-929A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AKIHVWIGLRAONKEKOCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCEO 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISENIQS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%; Score 404; DB 1; Length 134; 55.9%; Pred. No. 8.1e-37; Live 22; Mismatches 34; Indels
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APPLICANT: Kirby, Edward P.
APPLICANT: Feng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platele
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESONDENCE ADDRES: 1
ADDRESSEE: Temple University - Of The Common-
STREET: 406 University Services Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Pennsylvania
CONTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: COMPUTER: DISKETTE, 3.50 inch, 720 Kb
COMPUTER: Diskette, 3.50 inch, 720 Kb
COMPUTER: Libr PS/2
COMPUTER: Diskette, 3.50 inch, 720 Kb
COMPUTER: Diskette, 3.50 inch, 720 Kb
COMPUTER: Diskette, 720 Kb
COMPUTER: DIsk
                                                                                                                                                                                                                                                                                                                 NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERRNCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-549
TELER. No. 5336667e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                APPLICATION NUMBER: US/07/893,929A FILING DATE: 19920605 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 134 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 QDPFVCE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : { { | | ;
124 LNPFVCK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 71; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-893-929A-2
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61 --KYHVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPDFKKCFVLKKESEFKTWSNVYCE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYVEHVV--PPTKCFVLERQTEFRKWIAVN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.2%; Score 309; DB 1; Length 133;
47.3%; Pred. No. 2e-26;
Live 24; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                            APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,929A
FILING DATE: 19220605
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION UNBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     Sequence 9, Application US/07893929A
Patent No. 533667
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEX: No. 533667'e
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 133 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.3%
Matches 62, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Philadelphia
STATE: Pennsylvania
                                                                            121 QODPFVCE 128
                                                                                                                           119 OKHIFMCK 126
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                                                                                                                                                                                                                                     61 SAKIHVWIGLRAQNKEKOCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                     1 DCPSDWSSFKQYCYQIVKELKTWEDAERFCSEQANDGHLVSIESYREAVFVAELLSENVK 60
                                                                                                                                         1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                                                    Gaps
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                                                                                                    5;
                                            55.2%; Score 395; DB 1; Length 130; 54.7%; Pred. No. 7.6e-36; ive 22; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.2%; Score 395; DB 5; Length 130; Best Local Similarity 54.7%; Pred. No. 7.6e-36; Matches 70; Conservative 22; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Temple University - Of The Common-ADDRESSEE: Wealth System of Higher Education STREETS: 406 University Services Building CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19921201
CLASSIFICATION:
PRICOR APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
TOPOLOGY: line.~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-DOS
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                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                  121 QODPFVCE 128
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OPERATING SYSTEM:
                                                                    Local Similarity
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US-07-893-929A-7
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                                            Query Match
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 123 amino acids
AMINO ACID
                                                                                                         ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                   STATE: Pennsylvania
                      STREET: 40b ourrective Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QQDPFVCE 128
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                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYEHVV--PPTKCFVLERQTEFRKWIAVN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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47.3%; Pred. No. 2e-26;
tive 24; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kirby, Edward P.
APPLICANT: Firby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                              ATTLE OF INVENTION: Alboagregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
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The 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
"Medium TYPE: IBM PS/2
"MR-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
Sequence 9, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
APPLICATION NUMBER: 07/803,630
ATTORNEY AGENT INFORMATION:
NAME: Monaco, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/07893929A
Patent No. 533667
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 60
TELECOMONICATION INFORMATION: (215) 568-8383
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 133 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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119 CEFKFPFVCKA 129
                                                                                                                                                                                                                                                         CITY: Philadelphia
STATE: Pennsylvania
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Best Local Similarity
Matches 62; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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PCT-US92-10344-9
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US-07-893-929A-4
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CITY: P
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education STREET: 406 University Services Building CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
E: wealth System of Higher Education 406 University Services Building
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 30,000,000,000
FILING DATE: December: 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniell A.
RESISTRATION NUMBER: 30,480
RESISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                             Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                 COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,929A
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 YLTRYIMIGLRVQNKGQPC-----SSISYENLV-DPFECFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLJAQKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FUNCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsayo
APPLICANT: NAGANO, Mitsayo
APPLICANT: TANAKA, Akiko
APPLICANT: TSHII, Koichi
APPLICANT: SHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS
TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                        Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                   42; Indels
                                                                                                                                                                                                                                                                                                                                                            Query Match 40.1%; Score 286.5; DB 2; Best Local Similarity 43.0%; Pred. No. 5.5e-24; Matches 55; Conservative 22; Mismatches 42;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MRR-1996
CLASSIFICATION: 435
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APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08612840A; Patent No. 5856126; GENERAL INFORMATION:
                                                           NAME: NO. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                       TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LECURE: 705-1.
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114 QQHSFICK 121
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STREET: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TANAMOTO, Hiroshi
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: TANAKA, Akiko
APPLICANT: TOSHIL, Kolchi
APPLICANT: YOSHIMOTO, Ryota
APPLICANT: YOSHIMOTO, Ryota
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.8%; Score 292; DB 5; Length 123;
Best Local Similarity 46.9%; Pred. No. 1.3e-24;
Matches 60; Conservative 18; Mismatches 42; Indels
                                                                                                                                                                                NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-6883
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 122.02
ZIP: 222.02
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILLING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08612840A
Patent No. 5856126
                                                                                                                                                                                                                                                                                              TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QQDPFVCE 128
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                                             FILING DATE: 1
CLASSIFICATION:
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PCT-US92-10344-4
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December 8, 2003, 09:54:55; Search time 53.0743 Seconds (without alignments) 452.044 Million cell updates/sec
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1 DCSSDWSSYEGHCYKVFKQS......GFHKWENFYCEQQDPFVCEA 129
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(cgnz_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
(cgnz_6/ptodata/2/pubpaa/US06 PUBF PUBB.pep:*
(cgnz_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
(cgnz_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
(cgnz_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
(cgnz_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
(cgnz_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*
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(cgnz_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*
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(cgnz_6/ptodata/2/pubpaa/US096 PUBCOMB.pep:*
(cgnz_6/ptodata/2/pubpaa/US008 PUBCOMB.pep:*
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(cgnz_6/ptodata/2/pubpaa/US008 PUBCOMB.pep:*
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(cgnz_6/ptodata/2/pubpaa/US008 PUBCOMB.pep:*
(cgnz_6/ptodata/2/pubpaa/US008 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*
                                                                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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score distribution.		Description	Sequence 2. Appli	'n	'n	à	0	; ;	Ì	, ~	ī -	ì	Semience C annual	; c	,000	٠ 0	Sequence 30. Appl	
is defived by analysis of the total score	SUMMARIES	di	US-09-938-114-2	US-09-929-230-5	US-10-226-420-5	US-09-929-230-8	US-10-226-420-8	US-09-929-230-11	US-10-226-420-11	US-09-969-763-3	US-09-969-163-1	US-09-929-230-2	US-10-226-420-2	US-09-969-10	US-09-764-870-439	US-10-125-540-439	US-09-997-003-30	
SIS		DB	11	10	12	10	12	10	12	10	10	10	12	10	σ	15	12	
y anal		Match Length DB	129	152	152	144	144	158	158	149	126	151	151	110	154	154	166	
o payta	* Query	Match	100.0	66.7	66.7	60.7	60.7	54.1	54.1	40.1	38.0	36.9	36.9	31.3	28.2	28.2	28.2	
TS CIE		score	715	477	477	434	434	387	387	386.5	371.5	264	264	23.5	201.5	201.5	201.5	

264 223.5 201.5 201.5 201.5

Sequence 43. Appl	Semience 1182. An	200	200	12	1 -	753.	000	4	5	Sequence 1013. An	Sequence 1070. An	107	Sequence 1078. An	eque	Sequence 1080. An	Sequence 1070. An	Sequence 1077, Ap	Segmence 1078. An	Sequence 1079, An	Sequence 1080, Ap	Sequence 2, Appli	Sequence 1070, Ap	Seguence 1077. Ap	equer	eguer	Segmence 1080. An	equer	eduer	Sequence 347, App	
0S-09-9	US-09-925-301-11	US-09-764-870-280	US-10-125-540-2	US-10-015-219-173	US-10-015-219-1	5-297-753	US-10-241-220-	316-761-4	US-10-316-761-	25-301-1	22-217-1	22-217	22-217	22-217	22-217	US-09-833-26	US-09-833-263		US-09-833-263-	US-09-833-263-1	US-09-525-0	US-10-025-380-1	US-10-025-38	US-10-025-380	US-10-025-380	US-10-025-380-1	US-10-100-608B	. US-10-157-031-114	US-10-205-823-3	
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28.2	28.2	28.2	28.2	28.2	28.2	26.9	25.8	25.6	25.6	25.6	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	
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ALIGNMENTS

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TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE VENOM OF AGKISTRODON ACUTUS
                          COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/9/938,114
FILING DATE: 23-Aug-2001
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/">CLASSIFICATION: <a href="https://doi.org/10.1007/">CLASSIFICATION: <a href="https://doi.org/10.1007/">CLASSIFICATION: <a href="https://doi.org/">CLASSIFICATION: <a href="https://doi.org/">CURRENT</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

**APPLICATION NUMBER: 09/058,740

**FILING DATE: <UNKnown>
ATTORNEX/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Chen, Anthony C. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite 4700
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
US-09-938-114-2
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APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASEUSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
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                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
              TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10226420; Publication No. US20030157686A1; GENERAL INFORMATION: APPLICANT: Sheppard, Paul O.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/09929230 ; Patent No. US20020161203A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-5
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144 EINPFVCEA 152
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Best Local Similarity
Matches 83; Conserv
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US-10-226-420-5
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US-09-929-230-5
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                      Length 152;
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Best Local Similarity 64.3%; Pred. No. 7.1e-44;
Matches 83; Conservative 16; Mismatches 30; Indels
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Patent No. US20020161203A1;
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS;
FILE REFERENCE: 00-72
CURRENT APLICATION NUMBER: US/09/929,230;
CURRENT FILING DATE: 2001-08-13;
NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Sistrurus miliarius
US-10-226-420-5
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Best Local Similarity 58.63
Matches 75; Conservative
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144 EINPEVCEA 152
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US-10-226-420-8
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US-10-226-420-11
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Matches 6
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                                                                                                                                                                                                                                                  33; Indels
Sequence 11, Application US/09929230
Fatent No. US20020161203A1
FAPPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TILLE OF INVENTION: RATLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT ALPILOATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 11, Application US/10226420
Bublication No. US20030157686A1
GENERAL INFORMATION
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                         60.7%; Score 434; DB 12
58.6%; Pred. No. 3e-39;
ative 20; Mismatches
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; ORGANISM: Sistrurus miliarius
US-09-929-230-11
                                                                                                                                                                                              Query Match
Best Local Similarity 58.0%
Chest Local Similarity 58.0%
Conservative
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132 QQNLFMCK 139
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EKNLFVCK 153
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Sequence 3, Application US/09969763

Sequence 3, Application US/09969763

Publication No. US20020198363A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KITO, MORIKAZU
APPLICANT: KITO, MORIKAZU
APPLICANT: FUTAKI, FUMIE
APPLICANT: SUZUKI, EIICHIRO
APPLICANT: SUZUKI, EIICHIRO
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: YAMADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING THE FILE REFERENCE: 214760USO
CURRENT APPLICATION NUMBER: US/09/969,763
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                                                                                                                                                                                                                                                                               54.1%; Score 387; DB 12; Length 158; 52.3%; Pred. No. 4.2e-34; ive 25; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Indels
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43.0%; Pred. No. 3.1e-23;
Live 22; Mismatches 42
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 158
TYPE: PRT
ORGANISM: Sistrurus miliarius
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PRIOR PRIOR DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VERSION 3.1
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Best Local Similarity 43.0%
Matches 55; Conservative
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137 QQHSFICK 144
                                                                                                                                                                                                                                                                                                         Similarity
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TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH FILE REFERENCE: 214760US0
CURRENT APPLICATION NUMBER: US/09/969,763
CURRENT PILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: UP 2000-305279
PRIOR FILING DATE: 2000-10-04
80 FTS--MMIGLK--DLWKECKWQWSDDTKLDYKAWTRR--PYCTVMVVKTDRIFWFNRGCE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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APPLICANT: Bishop, Paul O.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.9%; Score 264; DB 12;
43.0%; Pred. No. 8.5e-21;
rative 18; Mismatches 49;
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; OTHER INFORMATION: SYNTHETIC PEPTIDE US-09-969-763-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09969763
Publication No. US20020198363A1
GENERAL INFORMATION:
APPLICANT: FUKUCHI, NACTUKI
APPLICANT: KITO, MORIKAZU
                                                                                                                                                                                                                         ; Sequence 2, Application US/10226420; Publication No. US20030157686A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KATO, MORIKAZU
KAYAHARA, TAKASHI
FUTAKI, FUMIE
ISHIKAWA, KOHKI
SUZUKI, ELICHIRO
GONDOH, KEIKO
SHIMBA, NOBUHISA
YAMADA, NAOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Sistrurus miliarius US-10-226-420-2
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SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 110
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Matches 55; Conservative
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134 KTVSFVCK 141
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US-10-226-420-2
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APPLICANT:
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APPLICANT: FUTAKI, FUMIE
APPLICANT: ISHIKAWA, KOHKI
APPLICANT: SUZUKI, EIICHIRO
APPLICANT: GONDOH, KEIKO
APPLICANT: GHIRBA, NOBUHISA
APPLICANT: SHIRBA, NOBUHISA
APPLICANT: AMADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.0%; Score 271.5; DB 10; Length 126; Best Local Similarity 41.4%; Pred. No. 1e-21; Matches 53; Conservative 22; Mismatches 44; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.9%; Score 264; DB 10; Length 151; 43.0%; Pred. No. 8.5e-21; tive 18; Mismatches 49; Indels
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APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT PLING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                    PILE REFERENCE: 214760US0
CURRENY PEPPLICATION NUMBER: US/09/969,763
CURRENY FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: JP 2000-305279
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.1
                                            ; Sequence 1, Application US/09969763; Publication No. US20020198363A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09929230 Patent No. US20020161203A1
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                                                                                                                APPLICANT: FUKUCHI, NAOYUKI
APPLICANT: KITO, MORIKAZU
APPLICANT: KAYAHARA, TAKASHI
APPLICANT: FUTAKI, FUMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Crotallus horridus
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114 QQHSFICK 121
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Matches 55; Conserv
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US-09-929-230-2
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61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENW-----IEEESKKCLGVHIETGFHK 113
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                                                                                                               -----CFMVSRDTRLREWFKVDCE 97
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28.2%; Score 201.5; DB 9; Length 154;
Best Local Similarity 28.9%; Pred. No. 5.2e-14;
Matches 39; Conservative 32; Mismatches 47; Indels 17; Gaps
  ch 31.3%; Score 223.5; DB 10; Length 110; l Similarity 35.2%; Pred. No. 1.4e-16; 45; Conservative 18; Mismatches 40; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 439, Application US/09764870
Fatent No. US202042386A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT TILING DATE: 2001-01-17
FULE REPERENCE: PTZ14
CURRENT TILING DATE: 2001-01-17
FULE SEC ILING DATE: 2001-01-17
FULE SEC IL NOS: 646
SEC IL NO 439
LENGTH: 154
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US-10-125-540-439
Sequence 439, Application US/10125540
Sequence 439, Application No. US2003059875A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14C1
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
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Query Match
Best Local Similarity
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LENGTH: 154
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; TYPE: PRT
; ORGANIEM: Homo sapiens
; REATURE:
; NAME/KEY: misc_feature
; LOCATION: (141)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-125-540-439
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                                                                                                                                                                                                                                                                                                                                1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                                                                                               Query Match 28.2%; Score 201.5; DB 15; Length 154; Best Local Similarity 28.9%; Pred. No. 5.2e-14; Matches 39; Conservative 32; Mismatches 47; Indels 17;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PA003P1
CURRENT APPLICATION NUMBER: US/09/997,003
CURRENT FILING DATE: 2001-11-30
FRIOR APPLICATION NUMBER: unassigned
PRIOR FILING DATE: 2001-11-30
FRIOR APPLICATION NUMBER: PCT/US00/22157
FRIOR APPLICATION NUMBER: PCT/US00/22157
FRIOR FILING DATE: 2000-08-11
FRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 56
SOFTWARE PATENTIN VET. 2.00
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28.2%; Score 201.5; DB 12; Length
Best Local Similarity 33.3%; Pred. No. 5.7e-14;
Matches 44; Conservative 26; Mismatches 53; Indels
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US-09-997-003-30
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- nucleic search, using frame_plus_p2n model
OM protein
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Run on:

December 8, 2003, 12:41:24 ; Search time 5475.5 Seconds (without alignments) 963.811 Million cell updates/sec

US-09-938-114-2

715 1 DCSSDWSSYEGHCYKVFKQS......GFHKWENFYCEQQDPFVCEA 129 **BLOSUM62** Scoring table: Title: Perfect score: Sequence:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

5777422 Total number of hits satisfying chosen parameters:

2888711 seqs, 20454813386 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

4: gb_on:*

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6: gb_pat:*

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em htg other: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result		Query				
No.	Score	Match	Length	8	QI	cription
н	0	8	733	Ŋ	17642	AF176420
5	2	91.9	497	Ŋ	175	91758 Deinagki
m ·	S)	ή.	959	ഹ	3	O Deinagki
47 r	ഗ	.i	544	9	AR259035	59035 Sequence
'n	ω,	٠. د	678	S	FIXA	Н
o t	496	•	683	S.	549	
` '	477	•	721	9	720	
ж (475	٠	630	2	AF190827	Gloydiu
φ.	460		632	Ŋ	530	
10	439	61.4	508	2	AF463522	522 Deinagk
1;	439	٠	199	Ŋ	64	G
12	4	•	580	9	AX427207	
13	420.5		408	Ŋ	0	Callose
14	397	55.5	456	9	AX427206	206 Seguence
15	394		477	Ŋ	AY099321	-
16	391		681	Ŋ	AY149341	341
17	m	54.1	725	φ	AX427210	210 Segment
18	380.5		495	Ŋ	AY091762	· ·
19	378		432	9	AX427209	Segment 6
20	377.5	52.8	704	2	AF102901	
21	375	52.4	508	Ŋ	AY091759	Deinagki
22	375		999	Ω	AF540645	
23		50.9	800	Ω	CDRNACVXA	Crotalus d
24	355.5		619	Ŋ	AB019615	AB019615 Agkistrod
25	329	46.0	474	9	AX427212	
26	291	Ö	698		TFLFIXB	н
27	290	。	634		AF197915	AF197915 Glovdius
28	290	ö	688		AF540647	Deinagk
29	289	ö	478		AY091761	Deinagki
30	9 9		069		AR026653	
31	286.5		069		AX404807	
32	e R		069		BD143687	587
	282		369		AY293866	3866
4 i	787	٠,	574		AF350324	50324
35	280	6	438	Ŋ	AF244901	901
36	278		458		AF176421	
3.7	277	m	592	Ŋ	588	381 Deinagki
38	274	œ,	478	2	AY091756	Deinagki
39	27	38.2	664	2	961	
40		÷.	583	Ŋ	ユ	AF125310 Gloydius
41	_:	œ,	œ	Ŋ	a	3521
42	m.	37.6	619	2	4	648 Deinagki
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44	264	36.9	738	Ŋ	CDRNACVXB	O.
45	5	35.8	484	w	AY091760	1760 Deinag

ALIGNMENTS

RESULT 1

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SIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCEQQDPFVCEA"
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/db xref="taxon:36307"
/clone="1210049"
/tissue_type="venom"
89. 547
/note="consists of two heterologous subunits (A and B chains) linked by an inter-subunit disulfide bond; c-type lectin family member"
            AF176420 T33 bp mRNA linear VRT 30-APR-2002 Deinagkistrodon acutus clone 2100490 agkisacutacin A chain mRNA,
                                                                                                                                                                                                                                                                                                       and
                                                                                                                                Deinagkistrodon acutus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Sclerogiossa; Serpentes; Colubroidea;
Viperidae; Croalinae; Deinagkistrodon.
(Dases I to 733)
Yu,H.-X., Xiang,K.-J. and Liu,J.
CDNA sequencing and analysis of eleven C-type lectin-like protein subunits from Agkistrodon acutus
Scheng wu hua hsueh yu sheng wu wu li hsueh pao (2002) In press (Dases I to 733)
Chang,X., Qian,Y., Liu,Q., Li,B.X.Y., Ding,J., Xu,Z., Huang,W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biology, University of Science and Technology of China, School of Life-Science, Huangshan Road, Hefei, Anhui 230027, China & Chaese I to 733)

Yu, H.-X., Xiang, X.-J., Wang, Y. and Liu, J.

Direct Submission

Submitted (23-APR-2002) Dept. of Biochemistry and Molecular Biology, University of Science and Technology of China, School of Life-Science, Huangshan Road, Hefei, Anhui 230027, China
                                                                                                                                                                                                                                                                                                                                      Agkisacutacin, a new fibrinolytic & anti-platelet protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 (bases 1 to 733)
Chengyx, Liu,J., Li,B.X.Y. and Qian,Y.
Direct Submission
Submitted (08-AUG-1999) Dept. of Biochemistry and Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence update by submitter
On Apr 23, 2002 this sequence version replaced gi:6715112
Location/Qualifiers
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Yu,H.-X., Xiang,K.-J., Wang,Y. and Liu,J.
A chain of agkisacutacin from Deinagkistrodon acutus
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1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20

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AY091758 497 bp mRNA linear VRT 13-MAY-2002
Deinagkistrodon acutus clone 2100590 ACF 1/2 A-chain mRNA, complete
                                                                                                                                                                                                                                                                                                                            457
218 AAGACCTGGACAGATGCAGAGGGGCTTCTGCACGAAGCAGGTGAACGGGGGGATCTGGTC 277
                                                                                                                                                                       278 TCTATCGAAAGCTCCGGAGAAGCAGACTTTGTGGGCCAGTTGATTGCTCAGAAGATAAAG 337
                                                                                                                                                                                                                                  81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
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                                                                                                                                                                                                                                                                                                            41 SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLyBIleLyB
                                                                                                                                                                                                              SerAlaLy81leHisValTrpIleGlyLeuArgAlaGlnAsnLy8GluLy8GlnCy8Ser
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A chain of ACF 1/2 from Deinagkistrodon acutus
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Yu,H., Xiang,K., Wang,Y. and Liu,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 CAACAGATCCTTTTGTCTGCGAGGCA 544
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Query Match:	91.33% Indels: 0	ORIGIN	
US-09-938-114-	GAPS: SR259035 (1-544)	t .:	Length:
Oy 10 Db 1	GluGlyHisCysTyrLysValPheLysGlnSerLysThrTrpThrAspAlaGluSerPhe 29 	Score: Percent Simi Best Local S Query Match:	96.00 5.97% 7.44% 9.37%
OY 30		DB: US-09-938-114	5 GAPS: -2 (1-129) x TFLFIXA (1-678)
-	Ilegly	Qy Db 11	1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysvalPheLysGlnSer 20
	erile 	Qy 2 Db 17	21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal 40
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QY 110	luala 	Qy 629	61 SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer 80 1917
SULT 5 LFIXA		9. E	81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
-	TFLFIXA 678 bp mRNA linear VRT 06-FEB-1999 Trimeresurus flavoviridis mRNA for factor IX/factor X binding protein A chain, complete cds.		
	D8331.1 GI:1402639 facotr IX/factor X binding protein A chain. Trimeresurus flavoviridis		
Ē	Illuctesulus lavovillus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Viparidsauris, Squabosa; Serpentes; Colubroidea;	SULT 6	
REFERENCE 1 AUTHORS Ma	(bases 1 to 678) Licalzaki,R., Yoshiara,E., Yamada,M., Shima,K., Atoda,H. and	Ž.	AB046491 Trimeresurus flavoviridis mRNA for factor XI/factor X binding
TITLE CI	Morica, I. cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant Droctein from snake venom	ACCESSION VERSION	procent a chain, compress cus. AB046491 GI:12583676
JOURNAL BI MEDLINE 96		S	Trimeresurus flavoviridis Trimeresurus flavoviridis
RS	· w		
TITLE DI JOURNAL SI BI	Direct Submission Submitted (02-FEB-1996) Takashi Morita, Meiji College of Pharmacy, Blochemistry; 1-22-1 Yatocho, Tanashi, Tokyo 188, Japan	REFERENCE	viperiode; Crocalinde; Illmeresulus. 1 (sites) Tani,A., Ogawa,T., Nose,T., Nikandorov,N.N., Deshimaru,M.,
(1) FEATURES	'el:0424-21-0101(ex.429), Fax:0424-21-1489) Location/Qualifiers form	TITLE	Chijiwa,T., Chang,C., Fukumaki,Y. and Ohno,M. Characterization and molecular evolution of an anticoagulant profein from Ackistrodon actus venom
	/organism="Trimeresurus flavoviridis" /mol_type="mRNA" /db_xref="taxon:88087"	JOURNAL REFERENCE AUTHORS	Unpublished 2 (bases 1 to 683) Ogawa. F. and Ohno. M.
5'UTR CDS	149 159 5.00. 508 7.00. atat-1	TITLE JOURNAL	Direct Submission Submitted (24-UUL-2000) Tomohisa Ogawa, Tohoku University, Dept. of Arrichitural Science. 1-1 Tentenmidori Amamiyamachi, Aoba-ku.
	/coun_scart_1 /product="factor IX/factor X binding protein A chain" /protein_id="BAA11887.1" /Ab_vref="GI-18405440"	REAUTTRES	Sendai, Miyagi 981-8555, Japan (E-mail:ogawa@biochem.tohoku.ac.jp, Tel:81-22-717-8807)
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Viperidae; Crotalinae; Sistrurus.
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Sistrurus miliarius
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Gloydius halys halyxin A-chain precursor (HXNA) mRNA, complete cds.
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KKOo,B.H., Sohn,Y.D., Kim,D.S., Jang,Y.S. and Chung,K.H.
Direct Submission
Submitted (29-SEP-1999) Cardiovascular Center, Yonsei University
College of Medicine, 134 Shinchon-dong, Seoul 120-752, Republic of
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Gloydius halys
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.

1 (bases 1 to 630)
Koo, B.H., Sohn, Y.D., Kim, D.S., Jang, Y.S. and Chung, K.H.
A novel coagulation factor Xa inhibitor from Korean snake
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Gloydius halys brevicaudus fibrinogen clotting inhibitor A chain
mRNA, complete cds.
AF125309
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AF463522 508 bp mRNA linear VRT 21-JAN-2002
Deinagkistrodon acutus antithrombin 1 A chain mRNA, complete cds.
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QCSSEWSDGSSVSYRNFFASTGTLGLELDSNYHKWYNVYCGQRNPFVCEA"
140 c 182 g 148 t
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Submitted (01-FEB-1999) Biochemistry, Yonsei University, Seodaemun
ku Shinchon dong 134, Seoul 120-749, Korea
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 CysteuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGluGln 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 TGTCTTGGGCTGGAACTGAACTCAAATTATCATAAGTGGGTCAATGTTTACTGGAAAA 471
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                          clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AlaLyslleHisValTrplleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSerIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34. .498
/codon start=1
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                                                                                                                        venom fibrin

    632
/organism="Gloydius halys brevicaudus"

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77
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Mismatches:
Indels:
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Purification and molecular cloning of
inhibitor
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Matches:
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/db_xref="taxon:66175"
/note="venom"
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Deinagkistrodon acutus agglucetin-alpha 2 subunit precursor, mRNA
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159 c 183 g 152 t
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Organism="Deinagkistrodon acutus"
/mol_type="mRRA"
/db_xref="taxon:36307"
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Mismatches:
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Lepidosauria, Squamata, Scleroglossa, St
Viperidae, Crotalinae, Deinagkistrodon.
1 (bases 1 to 661)
Wang, W.J. and Huang, T.F.
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3 (bases 1 to 661)
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                                                                             Deinagkistrodon acutus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.

(bases 1 to 508)

1, (hases 1 to 508)

1, Ainay, K. and Liu, J.

Direct Submission

Submitted (28-DEC-2001) Dept. of Biochemistry and Molecular
Biology, School of Life-Science, Huangshan Road, Hefei, Anhui
230027, China
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/note="C-type lectin family member"
                                                                                                                                                                                                                                                                                                                                             organism="Deinagkistrodon acutus"
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Mismatches:
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/trānslation="MGRFIFVSFGLLVVFLSLSGTGADFNCPPGWSAYDQYCYQVIKE
PKNWDDAERFCTEQADGGHLVSIESKGERDFVAQLVSQNIESVEDHVWTGLRVQNKEK
QCSTEWSDGSSVSYENLLELYMRKCGALERETGFHKWINLGCIQLNPFVCKFPPPQC"
                                                                                                                                                                                                                                                                        2 (bases 1 to 661)
Wang,W.-J., Ling,Q.-D. and Huang,T.-F.
Molecular structure and functional characterization of agglucetin,
a tetrameric glycoprotein 1b-binding protein, from Formosan pit
           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 AATTGTCCCCCTGGTTGGTCCGCCTATGATCAGTATTGCTACCAGGTCATCAAAGAACCG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang, W.-J., Ling, C.-D. and Huang, T.-F.
Direct Submission
Submitted (123-AUG-2002) Department of Nursing, Chang Gung Insti
of Technology, 261, Wen-Hwa I Rd., Kwei-Shan, Tao-Yuan, Taiwan
333-03, R.O.C.
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Craniata; Vertebiaca, ___oqlossa; Serpentes; Colubroidea;
                                                                                                                                               from Agkistrodon
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/note="platelet agglutination inducer; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /produčt="agglucetin-alpha 2 subunit precursor"
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/db_xref="GI:23321261"
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Calloselasma rhodostoma aggretin alpha chain mRNA, partial cds.
AF244900
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Chung, C.H., Au, L.C. and Huang, T.F.
Direct Submission
Submitted (11-MAR-2000) Pharmacology, College of Medicine, National Taiwan University, No. 1, Sec. 1, Jen-Ai Rd., Taipei, Taiwan Location/Qualifiers
              LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Calloselasma.

1 (bases 1 to 408)
Chung, C.H., Au, L.C. and Huang, T.F.
Molecular cloning and sequence analysis of aggretin, a molecular cloning and sequence analysis of aggretin, a biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biophys. Res. Commun. 263 (3), 723-727 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / organism="Calloselasma rhodostoma"
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/tissue type="venom gland"
/tissue type="venom gland"
/tissue fyme heterodimer of alpha and beta chains;
/note="forms heterodimer of alpha and beta ggregation;
similar to C-type lectins and glycoprotein 1b binding
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77
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Mismatches:
Indels:
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/protein id="AAF79952.1"
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Calloselasma rhodostoma
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/pootein_id="CAD35500.1"
/db_xref="G1:21530570"
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AKGGHIVSIESDGEARAVAQLVAENIKQNKYDVMIGLRIQGEEKQCSTKWSDGSSVNY
ENLIKHATKKCFGLKKETGFRTWRNVHCTQQNLFMCKFPPEC"
133 c 163 g 130 t
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGACGTGGGGACGATGCAGAGGTTCTGCTCGGAGGCGAAGGCGAAGGGCGGAAGGCTCTCGTC
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328 ACAGAGTGGAGCGATGGCTCCAGCGTCAGTTATGAGAACCTGCTTGAACTATATATGAGA
                                                                                                                         LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu
                                                                                                                                           81 lleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluSerLys
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Matches:
Conservative:
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/organia="Sistrurus miliarius"
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                              Sistrurus miliarius (pigmy rattlesnake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sheppard, P.O. and Bishop, P.D.
Rattlesnake venom gland proteins
Patent: WO 0214364-A 7 21-FEB-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Viperidae, Crotalinae, Sistrurus.
                                                                                                                                                                                                                                                                                      Sequence 7 from Patent WO0214364.
AX427207.1 GI:21530569
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                                                                                                                                                                                          GlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                            /codon_start=1
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/note="Zsnk4"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Protobothrops.

Welson 1 to 477.

Wel, Q., Lu, Q.M., Jin, Y., Li, R., Wei, J., Wang, W. and Xiong, Y. Purification and cloning of a novel C-type lectin-like protein with platelet aggregation activity from Trimeresurus mucrosquamatus
                                                                                                                                                                                                                                                 Protobothrops mucrosquamatus C-type lectin-like protein TMVA A chan, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="C-type lectin-like protein TMVA A chain"
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QCRSEWSDASSVNYENLFKQSSKKCYALKKGTELRTWFNVYCGRENPFVCKYTPEC"

100 c 134 g 121 t
                                                                                         101 LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                     370 ACNIGYYINGGNYINCARCARGGNACNAAYIAYCAYAARIGGGINAAYAIHTAYIGYGGN 429
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                        81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys
                                                      310 GCNAARTGGWSNGAYGGNWSNWSNGTNWSNTAYGARAAYTGGATHGARGCNGARWSNAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (23-APR-2002) Department of Animal Toxicology, Kunminstitute of Zoology, 32 East Jiaochang Road, Kunming, Yunnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Protobothrops mucrosquamatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="platelet aggregation activator"
/codon_start=1
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Mismatches:
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/isolation source="venom"
/db_xref="taxon:103944"
1. .477
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Protobothrops mucrosquamatus
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190 CTGGCAGACGAAGACTACGTCTGGATCGGACTCAAGGGCTCAAAAGAAGAAGAAGAATGC 249
                                                                    LysLysCysLeuGlyValHislleGluThrGlyPheHisLysTrpGluAsnPheTyrCys 119
                                                                                                                                                                                                                                                                        249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZymoGenetics, Inc. (US)

Location/Qualifiers

1. 456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_txref="taxan:32630"
/note="This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID No:5."

72 a 31 c 92 g 66 t 195 others
                                                 SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
                                                                                                                 61 SerAla----LyslleHisValTrplleGlyLeuArgAlaGlnAsnLysGluLysGlnCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
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Matches:
Conservative:
Mismatches:
Indels:
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Rattlesnake venom gland proteins
Patent: WO 0214364-A 6 21-PEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6 from Patent W00214364.
                                                                                                                                                                                                                                                                                                                     GluGlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                                                                                                                                                                     GAACAAATGCATGCTTTCGTCTGCAAG 396
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artificial sequences.
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DB:
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Search completed: December 8, 2003, 16:08:44 Job time : 5477.5 secs

121 GlnGlnAspProPheValCysGlu 128 :::::::::||||||||||:: 436 AGAGAAAATCCTTTCGTCTGCAAG 459

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	(without alignments) 786.026 Million cell updates/sec
Title:	US-09-938-114-2
Sequence:	11) 1 DCSSDWSSYEGHCYKVFKQSGFHKWENFYCEQQDPFVCEA 129
Scoring table:	BLOSUM62
	Xgapop 10.0 , Xgapext 0.5
	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0, Fgapext 7.0
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2552756 seqs, 1349719017 residues Searched:

5105512 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 10

Command line parameters:

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Database :

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and is derived by analysis of the total score distribution.

SUMMARIES Description		3 cDNA encodin	Pigmy rattle	2015 Shake venom blood	Pigmy rattles	Pigmy	Pigmy		Snake	Snake venom a	DNA encoding a sn	Korean adder	Pigmy rattles	1929 Shake Venom protein 1674 cDNA encoding Dein	Pigmy	Sequence encoding		CDNA sequence of	Human colon a	Human Himan	Human	Human polynuc	Human Human	Human Tumour	DNA encoding hum	Codin	Human	Sequen	Mirit	Murine E-sel	Mouse Tumour		MUREG-	Human reg cDNA. Human pancreati Human pancreati	ALIGNMENTS						•	us antithrombosis enzyme alpha chain.	in; fibrin hydrolysis; blood clot:	disorder; thromboembol	ncer; neurodegenerative disease;	mosts; chromboangilitis	ase; unscaple angina; acute inrombosis;
SU DI ID	-		24 AAU3205	24 ADI.4	24 AAD3	24 AAD3	24 AAD3	24 AAD3	22 AAI7	16 AAQ8	24 AAK9	24 AAL4	24 AAD3:	25 ABX9:	24 AAD3:	11 AAQ00	24 AB06(21 AAZ9	22 AAF7	22 AAF7	22 AAS3:	24 ABQ6	21 AAA93	24 ABL92	25 ABX72	25 ABZ34	24 ABZ11	9 AAN819	18 AAV02		44 14	21 AAA92454		10 AAN9110 24 ABV9509 24 ABV9826	ALI		:	544 BP.		_		odon acutus	alpha chain;	-	stenosis; erehral t	ar dispase.	1
Length		544	127	4 6 6	580	456	725	474	633	069	069	583	483	454	453	441	262	111	800	843	1066	1066	4771	5641	5641	5747	678	498	4588	4588	4588 4588	833	9	495 710 539				; cona;		st entry)		Deinagkistrodon	ss; PCR;	ion; vag	tion; re bosis: c	J vascular	^
% Query Match		91.3		6.43	60.7	55.5	54.1	46.0	40.6	40.1	40.1	38.1	36.9	30.2	29.4	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	27.8	27.6	27.6	27.6	27.6	27.6	27.5	27.3 27.1 26.9			4	standard;		3 (firs			s;sisc	ggregat	intarc c throm	cerebra	רכובחומו א
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thrombosis

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GGGTTTCATAAGTGGGAGAATTTTTACTGTGAACAACAAGATCCTTTTGTCTGCGAGGCA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                             181 CTGAGGCTCAAAACAAAGAAAAGCAATGCAGCATAGAGTGGAGGGATGGCTCCAGCATC
                                                                                                                                                                                                241 AGTTATGAGAATTGGATTGAAGAAGAATCCAAAAAGTGTCTTGGGGTGCACATAGAGACA
                                                                                                                                                                                                                                          GlypheHisLysTrpGluAsnPheTyrCysGluGlnGlnAspProPheValCysGluAla
                                                                                                                                                        SerLysGluAsnTrp1leGluGluGluSerLysLysCysLeuGlyValHisIleGluThr
                                                                   LeuArgAlaGlnAsnLysGluLysGlnCysSerIleGluTrpSerAspGlySerSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rattlesnake; venom gland protein; blood coagulation; therapy; et aggregation; gene; Zsnk3; ds.
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/product= "Mature Zsnk3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 73-74; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                       BP
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14-AUG-2000, 2000US-2250B7P.
15-AUG-2000, 2000US-22548BP.
15-AUG-2000, 2000US-22549BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-2001; 2001WO-US25310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sistrurus miliarius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenualy. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.005 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thrombosis, on significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thrombosis, including myocardial infarction, restenosis, angiopathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable agina, acute thrombosis, instable stenocardia, thrombosis, pulmonary embolism, deep vein thrombosis, peripheral arterial occulsion, stroke. It is also useful for treating atherosclerosis, oceans and inflammation, cancer and neurodegenerative diseases. The present sequence represents cDNA encoding the Deinagkistrodon acutus antithrombosis enzyme alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TGCACGAAGCAGGTGAACGGGGGGCATCTGGTCTTCTATCGAAAGCTCCGGAGAAGCAGAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 GluGlyHisCysTyrLysValPheLysGlnSerLysThrTrpThrAspAlaGluSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 CysThrLysGlnValAsnGlyGlyHisLeuValSerIleGluSerSerGlyGluAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
                                                                                                                                                            product= "Antithrombosis enzyme alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 544 BP; 158 A; 122 C; 143 G; 121 T; 0 other;
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0 0
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/note= "No start codon given"
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Mismatches:
Indels:
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Matches:
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                                                                                                Location/Qualifiers
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653.00
99.17%
99.17%
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                                                                                                                                                                                     partial
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'*tag=
                                                     Deinagkistrodon acutus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheng X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (HEFE-) HEFEI
                                                                                                                                                                                                                                                                     US6489451-B1
                                                                                                                                                                                                                                                                                                                                                        10-APR-1998;
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unstable

BX,

Query Match:

셤 8

8

CO LTD

BIOBUD

(BIOB-)

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polynucleotide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland protein, Zsnk3 gene.
   888888888888888
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C; 203 G; 159 T; 0 other; BP; 192 A; 167 Sequence 721

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339
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                                                                                                                                                                                                                                                      459
                                                                                                                                                                                                                                                                    101 LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                                                                                                         519
                                                                                      AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                             40
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                                                                                                                                                                              TCTATCGAAAGCTCCGAAGAAGCAGCCTTTGTGGCCCCAGCTGGTCCCTGAGAACAGGAGG
                                                                                                                                                                                                                                 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys
                                                                                                                                                                                                                                            SerileGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
                                                                                                                                                                                              SeralaLys1leHisValTrpileGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                          LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                             Snake venom blood anticoagulant halyxin A chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               pit viper; venom; halyxin; anticoagulant; thrombogenesis;
           721
83
16
30
0
                           Conservative:
Mismatches:
           Length:
Matches:
                                              Indels:
                                                                                                                                                                                                                                                                                                      GlnGlnAspProPheValCysGluAla 129
                                                                                                                                                                                                                                                                                                                  GAAATAAATCCTTTTGTCTGCGAGGCA 546
                                                     Gaps:
                                                                      x AAD32055 (1-721)
                                                                                                                                                                                                                                                                                                                                                            BP
         1.04e-47
477.00
76.74%
64.34%
66.71%
                                                                                                                                                                                                                                                                                                                                                           AAI71876 standard; DNA; 601
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                     US-09-938-114-2 (1-129)
                                  Best Local Similarity:
                         Percent Similarity:
Alignment Scores:
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                                            Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
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                                                                                                                                                                                                                                                                                                                                                  AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                           GATTGTCCCTCTGGTTGGTCCTCCTATGAAGGCCATTGCTACAACATCTTCCATCTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 ACGIGICTIGGGCTGCAAAAGAGACAGAGTTTCGTAAGTGGTTTAATATTACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 AGATACGGGATCTATATCTGGATCGGGCTTCGAGGCTAAAAGAAGAAGCAATGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 TCCCAGTGGAGCGATGGCTCCAGCGTCAGTTATCAGAACTGGATGAAGCAGAAATCCAAA
                                                                                                                        blood anticoagulation activity. The protein with very strong venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence encodes the A chain of halyxin.
                                                                                                                                                                                                                                                                                                                                                                                                   LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                        venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Korean adder snake venom salmorin A chain protein cDNA sequence.
                                                                                Halyxin as blood anticoagulation protein separated from snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korean adder; ss; salmorin protein A chain; snake venom;
fibrinogen clotting inhibition; thrombosis; prothrombin thrombin binding; blood coagulation.
                                                                                                                                                                                                        Sequence 601 BP; 166 A; 133 C; 163 G; 139 T; 0 other
                                                                                                                                                                                                                                             601
17
17
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                           Son
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                                                                                                                                                                                                                                                                                                                              (1-601)
                          Koo BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                             US-09-938-114-2 (1-129) x AAI71876
                                                                                                           Claim 1; Page 9; 21pp; Korean
                                                                                                                                                                                                                                        1.41e-47
475.00
76.74%
63.57%
66.43%
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                         Kim DS,
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                                               2001-637330/73
                         Jung GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL42015 standard;
                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                           P-PSDB; AAM51543
                                                                                                                                                                                                                                Alignment Scores:
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                       Jang YS,
                                                                                                                                                                                                                                                                                                                                                                                                   21
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DB:
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Agkistrodon halys brevicaudus

29-JUN-2000; 2000KR-0036591

Agkistrodon halys thrombosis; ds.

KR2001049671-A

15-JUN-2001

99KR-0025105

29-JUN-1999;

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GluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGerLysLys 101
                             rererresecresaacrasacreaarrarearasegesecaarstracreresacaa 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new pigmy rattlesnake (Sistrurus miliarius) wenom gland proteins, which affect blood coagulation and platelet aggregation system. The polypeptides, which affect blood coagulation and platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory practical kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The
                                                                        CysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGluGln
                                                                                                                                                                                                                                                                                                                                                Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; gene; Zsnk4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, affect blood coagulation and platelet aggregation system, useful itherapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                       Pigmy rattlesnake venom gland protein, Zsnk4 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
30..434
/*tag= c
/product= "Mature Zsnk4 protein"
                                                                                                                                                                   495
                                                                                                                                    GlnAspProPheValCysGluAla 129
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                           AGAAATCCTTTCGTCTGCGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Zsnk4
/note= "CDS does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 75; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-225072P.
2000US-225087P.
2000US-225489P.
2000US-225490P.
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                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .437
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P-PSDB; AAE20180.
                                                                                                                                                                                                                                                                                                                                                                                                     Sistrurus miliarius.
                                                                                                                                                                                                                                AAD32057 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200214364-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000;
15-AUG-2000;
15-AUG-2000;
20-DEC-2000;
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              82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGAAACACGGGCAGAAGCAGACTTTGTGGCCCACGTGGTCGCTGAGAGGAGGATAGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New salmorin protein derived from venom of Korean adder Agkistrodon halys brevicaudus, useful for treating thrombosis by repressing fibrinogen clotting through repression of activation of prothrombin
                                                                                                                                      Salmorin A chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 162 A; 140 C; 182 G; 148 T; 0 other;
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77
20
31
0
                                             "Salmorin A chain protein"
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Matches:
Conservative:
Mismatches:
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                                                                        /*tag= b
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-938-114-2 (1-129) x AAL42015 (1-632)
cocation/Qualifiers
                                                                                                                         /*tag= c
'note= "Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1A; 30pp; English.
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460.00
75.78%
60.16%
64.34%
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                                                                                                                                                                                                                                                                                                                         27-JUL-2000; 2000KR-0043470
                                /*tag= a
/product=
                                                                                                                                                    499..622
/*tag= d
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623..632
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                                                                                                                                                                                                                                                                                                                                                        (BIOB-) BIOBUD CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                      Kim D,
                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AA014520
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                                                                                                                                                                                                                                  WO200214514-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into thrombin
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                                                               sig peptide
                                                                                                          mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                        Chung K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
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polynucleotide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichrolism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                            protein, Zsnk4 gene.
   88888888888
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Sequence 580 BP; 154 A; 133 C; 163 G; 130 T; 0 other;

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155
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                                                                                                                                                                                                                                                                                                                                                        LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                                                                                                                                                                                               336 AAGIGITTTGGGCTGAAAAAGAGACAGGTTTCGCACGTGGCGCAATGTTCACTGTACA 395
                                                                                                                     AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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                                                                                                                                 61 SerAlaLysIleHisValTrpileGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                         81 lleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys
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              580
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33
            Length:
Matches:
Conservative:
Mismatches:
                                                           Indels:
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                                                                                          US-09-938-114-2 (1-129) x AAD32057 (1-580)
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            1.12e-42
434.00
74.22%
58.59%
60.70%
                                  Percent Similarity:
Best Local Similarity:
Alignment Scores:
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Pigmy rattlesnake venom gland protein Zsnk3, degenerate nucleic acid.
                                                                                        rattlesnake; venom gland protein; blood coagulation; therapy; et aggregation; ds.
                   ВР
                  AAD32056 standard; DNA; 456
                                                                                                                                                                        13-AUG-2001; 2001WO-US25310
                                                      (first entry)
                                                                                                 platelet aggregation;
                                                                                                                   Sistrurus miliarius
                                                                                                                                    WO200214364-A2
                                                     18-JUN-2002
                                   AAD32056
RESULT 6
          AAD32056
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189

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310 GCNAARTGGWSNGAYGGNWSNWSNGTNWSNTAYGARAAYTGGATHGARGCNGARWSNAAR 369 LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120

엄 à d 121 GlnGlnAspProPheValCysGluAla 129

14-AUG-2000; 2000US-225072P.

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
protein chemistry and antibody production and analysis. The
polynucleotide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
protein by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein Zsnk3, degenerate nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 SerileGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 WSNATHGARWSNWSNGARGARGCNGCNTTYGTNGCNCARYTNGTNCCNGARAYMGNMGN
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                                                                                                                                                                                                                  New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                     Disclosure; Page 74; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-114-2 (1-129) x AAD32056
15-AUG-2000; 2000US-225489P.
15-AUG-2000; 2000US-225490P.
20-DEC-2000; 2000US-356997P.
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397.00
59.69%
51.16%
55.52%
                                                                                INC.
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                                                                                                                     Bishop
                                                                              (ZYMO ) ZYMOGENETICS
                                                                                                                                                          2002-269180/31.
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Best Local Similarity:
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                                                                                                                     Sheppard PO,
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AAD32059;

RESULT 7 AAD32059 Key

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LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                                                                                                                                                         163 AATTGTCCCTCTGGTTGGTTCGCCTACGATCAGTATTGCTACAGGGTCATCAAACGACTC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 CAAAACCAATACTATGTCTGGATTGGACTGAGGATTCAAAACAAAGGACAGCAATGCAGC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 IleGluTrpSerAspGlySerSerIleSerLysGluAanTrpIleGluGluSerLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 ACGAAGTGGAGGGATGGCTCCAGCGTCAGTTATGAGAACCTGGTTAAATCACATTCCAAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||::||||::|||
rctgtcgaaaacgatgaagcagtctttctggcccagttggtcgctgcgaacataaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rattlesnake; venom gland protein; blood coagulation; therapy;
                                                             Conservative:
                                                                                                   Mismatches:
Length:
Matches:
                                                                                                                                     Indels:
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                                                                                                                                                                                                                                  US-09-938-114-2 (1-129) x AAD32059 (1-725)
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14-AUG-2000; 2000US-225087P.
15-AUG-2000; 2000US-225499P.
15-AUG-2000; 2000US-225490P.
15-AUG-2000; 2000US-356997P.
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                              387.00
71.88%
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54.13%
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                                                                                                   Best Local Similarity:
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                                                                 Percent Similarity:
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                                                                                                                                     Query Match:
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      Pred. No.:
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venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
practical kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The polymelectide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
porting purposes. The polypeptides are also useful in identifying
for testing purposes are polypeptides are also useful in identifying
to protein by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. Zenk5 gene.
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                                                                                                                                                                                                                                                                                                                                                                                               Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; gene; Zsnk5; ds.
                                                                                                                                                                                                                                                                                                                                  Pigmy rattlesnake venom gland protein, Zsnk5 gene.
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157..561
/product= "Mature Zsnk5 protein"
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/product= "Zsnk5 protein"
      430 GARATHAAYCCNTTYGTNTGYGARGCN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000; 2000US-225087P.
15-AUG-2000; 2000US-225489P.
15-AUG-2000; 2000US-225490P.
20-DEC-2000; 2000US-356997P.
                                                                                                                                     AAD32059 standard; DNA; 725
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                                                                                                                                                                                                                                                                 (first entry)
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P-PSDB; AAE20181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sistrurus miliarius.
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New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or WPI; 2002-269180/31.

Sequence 725 BP; 179 A; 171 C; 200 G; 175 T; 0 other;

Alignment Scores:

us-09-938-114-2.rng

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
protein chemistry and antibody production and analysis. The
polymuclectide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
for testing purposes. The polypeptides are also useful in identifying
protein by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein Zsnk4, degenerate nucleic acid.
                                                    Disclosure; Page 76; 79pp; English
molecular biology
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Sequence 432 BP; 91 A; 34 C; 84 G; 55 T; 168 other;

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81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluSerLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                   LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                                                 94 MGNACNIGGGAYGAYGAYGARMGNTIYIGYWSNGARCARGCNAARGGNGGNCAYYTNGIN 153
                                                                                                                                                                                                                                                                                                                                               214 CARAAYAARTAYGAYGTNTGGATHGGNYTNMGNATHCARGGNGARGARAARCARTGYWSN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 AARTGYTTYGGNYTNAARAARGARACNGGNTTYMGNACNTGGMGNAAYGTNCAYTGYACN 393
                                                                                                                                                                                                                                                                                                                      SerAlaLysIleHisValTrplleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer 80
                                                                                                                                                                        34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGYTAYMGNGTNATHAARCARYTN 93
                                                                                                                                           1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                   41 SerileGluSerSerGlyGluAlaAspPheValGlyGlnLeulleAlaGlnLysileLys
                                                                                                                                                                                                                                                                                                                                                                                                  21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                   432
64
16
48
0
                  Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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               3.96e-36
378.00
62.50%
50.00%
52.87%
                                                          Similarity:
                                           Percent Similarity:
Alignment Scores:
Pred. No.:
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                                                                     Query Match
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polyreptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide an be used as standards or as unknowns
polymucleotide or polypeptide and be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
proteins by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                          New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, affect blood coagulation and platelet aggregation system, useful itherapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 78; 79pp; English
                                                                                                                                                                   2000US-225087P.
2000US-225489P.
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329.00
58.59%
42.97%
                                                                                                                13-AUG-2001; 2001WO-US25310.
                                                                                                                                                    2000US-225072P.
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20-DEC-2000; 2000US-356997P.
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                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                           PD;
                                                                                                                                                                                                                                                                                         Sheppard PO, Bishop
              Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                           WPI; 2002-269180/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                            molecular biology
                                              WO200214364-A2
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136 AARACNIGGGAYGAYGCNGARMGNIIYIGYWSNGARCARGCNAARGGNGGNCAYYINGCN 195

21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal

8 엄 ò 셤 ð

96 WSNGTNGARAAYGAYGARGARGARGTNTTYYTNGCNCARYTNGTNGCNGCNAAYATHAAR 255

41 SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysileLys

SerAlaLys1leHisValTrp1leGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer 80

61

Pigmy rattlesnake venom gland protein Zsnk5, degenerate nucleic acid. Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;

platelet aggregation; ds

(first entry)

18-JUN-2002

AAD32060

AAD32060 standard; DNA; 474

RESULT

RESULT

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101 LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                           CACGGTATTTTC-----TGGATGGGACTG-----AGCAATGTCTGGAATCAATGCAGC 320
                                                                                                             81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
                                                                                                                                            321 TGGCAATGGAGCAGTGCTGCCAAGCTCAAATACGAAGCCTGGGCTGAAGAA-----TCT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR71978 and AAR71979 are snake venom derived antithrombotic peptides, specifically from the snake venom oligopeptide AAR71981, encoded by AAQ89309. These peptides have the advantage of avoiding significant thrombocytopenia when administered at the minimum dose, for in vivo inhibition of platelet von Willebrand factor binding.

(Updated on 25-MAR-2003 to correct PN field.)
                                               61 SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antithrombotic peptide; snake venom; platelet binding inhibition; von Willebrand factors; Crotalus horridus horridus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single-chain antithrombotic peptide - obtained by cleaving an oligopeptide from snake venom to break inter-chain disulphide bonds but preserve intra-chain disulphide bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Snake venom antithrombotic oligopeptide cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kito M, Kobayashi T,
, Yoshimoto R;
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Matches:
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                                                                                                                                                                                                                                       GlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                                                                                     429 ATGGAGGCATATTTCGTCTGCGAG 452
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66..515
/*tag= a
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286.50
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(first entry)
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Yamamoto H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-139559/18.
P-PSDB; AAR71981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1993;
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28-NOV-1995
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                                                                                 273
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Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212
                                                                                                  435
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                                                                  LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
      81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys
                             AARTGYTTYGGNYTNAARAARGARACNGARTTYYTNCARTGGTAYAAYACNGAYTGYGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to halyxin, a novel protein with very strong blood antioorgulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                  Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
                                                                                                                                                                                                                                                                                                                      Snake venom blood anticoagulant halyxin B chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 633 BP; 179 A; 142 C; 157 G; 155 T; 0 other;
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633
646
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Matches:
Conservative:
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Indels:
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                                                                                                                                 GlnGlnAspProPheValCysGlu 128
                                                                                                                                                    GARAARAYYTNTTYGTNTGYAAR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the B chain of halyxin.
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290.00
57.81%
46.09%
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                                                                                                                                                                                                                              AAI71877 standard; DNA; 633
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                                                                                                                                                                                                                                                                                        (first entry)
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                   Agkistrodon halys.
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                                                                                                                                                                                                                                                                                                                                                                     thrombosis; ds.
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                                                                                                                                         LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal 40
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                                                                                       AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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TCTGTCGAAACCGCCCTAGAAGATCTTGTGGACAATGTGCGAACAAAGAG
                                                                                                                                                                                                                                                                                              81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys
                                                                                                                                                                                                                                                                                                                                                                        GAATGITITATGGTGAGCAGAGACACAAGGCTTCGTGAGTGGTTTAAAGTTGACTGTGAA
                                                                                                                                                                    ATGACCTGGGCCGATGCAGAGGTTCTGCTCGGAGCGAGGCGAAGGCGGCGATCTCCTC
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                                                                                                                                                                                                                                              SerAlaLys1leHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
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                                                                                                                                                                                                                                                                                                                                                   LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing physiologically-active subunit peptides originating in polymer proteins by denaturation and specific separation, with lower antigenicity but improved solubility and stability, e.g. blood platelet-binding inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subunit peptide production, snake venom; rattlesnake, thrombolytic, von Willebrand's factor; blood platelet-inhibitory activity, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a method for the production of a subunit
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    2462
  Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding a snake venom derived protein.
                                       Gaps:
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                                                                x AAQ89309 (1-690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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 60.16%
42.97%
40.07%
16
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                                                             US-09-938-114-2 (1-129)
Percent Similarity:
Best Local Similarity:
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                        Query Match
DB:
             Best Local
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peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its subunit using a protein denaturing agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity on von Willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents method of the invention.
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antigenicity;
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/*tag= a
/product= "Antithrombotic wild-type rattlesnake protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SerAlaLys1leHisValTrp1leGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 GAATGITITATGGTGAGCAGAGACACAAGGCTTCGTGAGTGGTTTAAAGTTGACTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------GACCATCAGATTATGAGAACCTGGTT-----GACCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding the antithrombotic wild-type rattlesnake protein.
                                                                                                                                                                                                  Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                 690
55
22
42
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; snake
half life; low
                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombolytic, glycoprotein Ib-binding antithrombotic, glycoprotein Ib; long drug efficacy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                                                                                                                                                                       US-09-938-114-2 (1-129) x AAC61144 (1-690)
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286.50
60.16%
42.97%
40.07%
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                                                                                                                                                                                                                                                                                             Best Local Similarity:
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DB:
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(first entry)

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16-MAY-2002
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81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 ATGACCTGGGCCGATGCAGAGATTCTGCTCGGAGCGAGGCGAAGGGCGAGGCGATCTCCTC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 GAATGTTTTATGGTGAGCAGAGACACAAGGCTTCGTGAGTGGTTTAAAGTTGACTGTGAA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer 80
                                                                                                                                                                                                                                                                                   The invention relates to a glycoprotein 1b-binding protein, originating from snake venom, comprising specific mutations and antithrombotic activity. Glycoprotein Ib-binding protein is used in a drug having antithrombotic activity. Glycoprotein Ib-binding protein has a high binding activity to glycoprotein Ib-binding protein has a high binding activity to glycoprotein Ib, a long half life/drug efficacy retention in blood, and low antigenicity. This polynucleotide sequence represents DNA of the wild-type rattlesnake protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                       Glycoprotein Ib-binding protein, useful for treating thrombosis, comprises specific mutations in protein originating from snake venom
                                                                                                                                          Ξ,
                                                                                                                                            Suzuki
                                                                                                                                            Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TCCAGCATCAGTTATGAGAACCTGGTT-
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                            Futaki F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x AAK99834 (1-690)
                                                                                                                                                                                                                                                             Example 1; Page 25; 49pp; English.
                                                                                                                                          Kayahara T,
Yamada N;
                                                                                                                                                                                                                                                                                                                                                                                                                            7.13e-25
286.50
60.16%
42.97%
                                                                                         04-OCT-2000; 2000JP-0305279
                                                                                                                  (AJIN ) AJINOMOTO CO INC
                                                                                                                                          Kito M,
Shimba N,
                                                                                                                                                                               2002-364482/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                 04-OCT-2001;
             EP1195384-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                       10-APR-2002
                                                                                                                                        Fukuchi N,
                                                                                                                                                        Gondoh K,
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DB:
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AAL42016
ID AAL420
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à qq à Ω à d à 셤 à 엄 à AAL42016 standard; cDNA; 583 BP

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The invention comprises the nucleotide and protein sequences of a salmorin protein derived from the venom of Korean adder. Salmorin protein is composed of an A chain and a B chain, and has inhibitory activity against fibrinogen clotting. The salmorin protein of the invention is useful for treating thrombosis, as it represses fibrinogen clotting potently by binding to prothrombin and thrombin so as to delay blood coagulation. The present cDNA sequence encodes the Korean adder salmorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New salmorin protein derived from venom of Korean adder Agkistrodon halys brevicaudus, useful for treating thrombosis by repressing fibrinogen clotting through repression of activation of prothrombin into thrombin
                              Korean adder; ss; salmorin protein B chain; snake venom; fibrinogen clotting inhibition; thrombosis; prothrombin binding; thrombin binding; blood coagulation.
adder snake venom salmorin B chain protein cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                        chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 G; 145 T; 0 other;
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114
9 49
8 9
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                         peptide
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                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                     /*tag= b
/note= "Signal
                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "Mature
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                                                                                                                       Agkistrodon halys brevicaudus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.72e-23
272.50
54.69%
43.75%
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/*tag= a
/product= '
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571..583
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                                                                                                                                                                                                                                                  sig_peptide
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    Korean
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                                                                              256 CACGGTATTTTC----TGGATGGGACTG-----AGCAATGTCTGGAATCAATGCAGC 303
                                                                                                                                                    81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
                                                                                                                                                                                              LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                             ---AICTAITIGIGICIAITICAAGICAACTAATAACAAAIGGAGGAGAGAGIAGAGCCIGCAGA 408
                                                                                                                80
                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
                                                                SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
                                                                                                           SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                      LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                 protein; blood coagulation; therapy;
                                                                                                                                                                         304 TGGCAATGGAGCAATGCTGCCAAGCTCAAATACGAAGCCTGGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not include start codon"
                                                                                                                                                                                                                                                                                                                                                                          Pigmy rattlesnake venom gland protein, Zsnk2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mature Zsnk2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Zsnk2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                           platelet aggregation; gene; Zsnk2; ds
                                                                                                                                                                                                                                          121 GlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Zsnk2
/note= "CDS does
                                                                                                                                                                                                                                                                                                                                                                                                rattlesnake; venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000; 2000US-225687P.
15-AUG-2000; 2000US-225489P.
15-AUG-2000; 2000US-225490P.
20-DEC-2000; 2000US-356997P.
                                                                                                                                                                                                                                                                                                          AAD32053 standard; DNA; 483
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60..455
/*tag= c
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/product=
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3..59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..458
                                                                                                                                                                                                                                                                                                                                                                                                                              Sistrurus miliarius.
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P-PSDB; AAE20178.
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
platelet aggregation system, are useful in therapy and diagnostics. The
platelet aggregation system as educational tool in laboratory
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
proteins by western blotting protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein, 2snk2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AAAACCTGGGATGATGCAGAGATTTCTGCTACACACAGAGACAGAGACAGCCGCCTGGCC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 TATTGTACAGTAATGGTAGTCAAGACAGATAGGATCTTTTGGTTCAATAGAGGTTGCGAA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SerAlaLysIleHisValTrplleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 TTCACTTCC-----ATGTGGATCGGACTGAA-----GATCTATGGAAAGAATGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::|||||||||||||||||:::
288 TGGCAGTGGAGGCATGACAACTGGACTACAAAGCCTGGACTCGAAGA-----CCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 SerileGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
  coagulation and platelet aggregation system, useful in itagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 483 BP; 129 A; 112 C; 123 G; 119 T; 0 other;
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55
18
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                           Claim 5; Page 71-72; 79pp; English.
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57.03%
42.97%
36.92%
                      diagnostics,
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                                      molecular biology
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affect blood
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                      therapy and
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Sequence 5, Appli Sequence 12, Appli Sequence 12, Appli Sequence 6, Appli Sequence 12, Appli Sequence 2, Appli

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Perfect score:

Title:

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Run on:

Scoring table:

Searched:

Sequence Sequence

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Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

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8

Patent No. Sequence 8

Sequence

Sequence Sequence Sequence

Sequence

Sequence 733, App

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TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE VENOM OF AGKISTRODON ACUTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09058740
Patent No. 6489451
GENERAL INFORMATION:
APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and Hui-Ran Chen
                                    US-08-822-261-5
US-09-226-852-5
US-08-822-261-6
US-08-822-166-12
US-09-146-969-2
US-09-226-852-6
US-08-612-840A-6
US-08-612-840A-6
US-08-612-840A-6
US-08-612-840A-6
US-08-612-840A-6
US-08-162-508-1
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US-09-620-312D-733
                                                                                                                                                                                                                                                   US-08-822-261-2
US-09-226-852-2
US-08-220-603A-1
US-08-365-103B-3
US-08-365-103B-3
US-08-365-103B-5
                                                                                                                                                                                    PCT-US95-07169-1
US-08-909-725-4
US-09-146-969-3
                                                                                                                                                                                                                          US-08-401-530A-1
US-08-709-662-1
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US-07-778-156-8
US-08-422-166-8
US-07-778-156-1
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                       US-08-422-166-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Chen, Anthony C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        storage
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ZIP: 90071-2066
RESULT 1
US-09-058-740-1
161.5
159
159
159
159
157.5
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-Delcapa 1/USD9303114/runat 08122003 091001 22878/app query.fasta_1.725
-Q=/Capa_1 1/USPTO spool/US09303144/runat 08122003 091001 22878/app query.fasta_1.725
-DB=IBSUGA_PATENTS = STRAT=1 - FND=-1 - MATRIX=DIOSUMG2 - TRANS=human40.cdi
-LOOPRAT=0 -UNITS-EDIAS -STRAT=1 - END=-1 - MATRIX=DIOSUMG2 - TRANS=human40.cdi
-LIST-45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-ELCAL - OUTFWT=120 - NORMEAX - HEAPSIZE=500 - MINLEN=0 -MAXLEN=200000000
-USER=US09938114 @CGN 1 1 95_@runat -08122003 091001 22878 - NCFU-6 - ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT - DSPELOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT - DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 12, Appli
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                                                                               December 8, 2003, 13:49:04; Search time 101.726 Seconds (without alignments) 559.725 Million cell updates/sec
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                                                                                                                                                             1 DCSSDWSSYEGHCYKVFKQS......GFHKWENFYCEQQDPFVCEA 129
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Sequence 1, A
Sequence 1, A
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                       - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-058-740-1
US-08-612-840A-7
US-09-058-740-12
US-09-146-969-1
US-08-840-062-3
US-08-840-062-3
US-08-454-557C-32
US-08-454-557C-32
US-08-450-673C-32
PCT-US95-17111A-32
US-08-340-428B-1
PCT-US93-07306-1
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                                                                                                                                                                                                                                                                      569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length
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653 286.5 216.5 201.5 201.5 197.5 195.5 195.5 184.5

Score

Result

Database :

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Query Match:
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: TANAKA, Akiko
APPLICANT: TRNAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: SHII, Koichi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY FITLE OF INVENTION: METHOD OF PRODUCING THE SAME
CORRESPONDENCE: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            544
1119
0
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0
                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
             REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPRONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-350
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-938-114-2 (1-129) x US-09-058-740-1 (1-544)
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                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 1:
REGISTRATION NUMBER: 38,673
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Patent No. 5856126
GENURAL INFORMATION:
APPLICANT: PUKUCHI, Naoyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T: FUKUCHI, Naoyuki
T: YAMAMOTO, Hiroshi
T: NAGANO, Mitsuyo
T: KITO, Morikazu
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99.17%
99.17%
91.33%
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ZIP: 22202
COMPUTER READABLE FORM:
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CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                           Alignment Scores:
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201 ATGACCTGGGCCGATGCAGAGGTTCTGCTCGGAGCAGCGAAGGGCGGCATCTCCTC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 GAATGITTTATGGTGAGGAGAGACACAAGGCTTCGTGAGTGGTTTAAAGTTGACTGTGAA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 GAATGTCCCTCCGGTTGGTCTTCCTATGATCGGTATTGCTACAAGAGCCCTTCAAACAAGAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeulleAlaGlnLysIleLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
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Mismatches:
Indels:
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Matches:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
TILING DATE: 20-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEFAK: 703-413-3000
TELEFAK: 703-413-3000
TELEFAK: 703-413-3000
TELEFAK: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Crotalus horridus horridus
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60.16%
42.97%
40.07%
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US-08-612-840A-7
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246 ----
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ORGANISM: HOMO
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US-09-146-969-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGIH: 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeu---
                                                                                                                                    THE SNAKE
                                                                                                                                 TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
3...440
OTHER INFORMATION: "N" stands for any base.
"Xaa" stands for any amino acid.
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                        APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and Hui-Ran Chen
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Chen, Anthony C.
REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
             Sequence 12, Application US/09058740 Patent No. 6489451 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                           storage
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INFORMATION FOR SEQ ID NO: 12:
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216.00
49.63
37.04
30.21
                                                                                                                                                              NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  STATE: California
                                                                                                                                                                                                                                     CITY: Los Angeles
                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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Query Match:
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US-09-058-740-12
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245
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                                                                                                                                                                        94 TrplleGluGluGluSerLysLysCysLeuGlyValHisIleGluThrGlyPheHisLys 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 IleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLysSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSerIle 81
                                                                    54 LeulleAlaGlnLysIleLysSerAlaLysIleHisValTrpIleGlyLeuArgAlaGln
                                                                                                              ---ÀAGTTGÀÀACTGATTAGTCTG------ÀTTGGÀCTGAAG-----
                                                                                                                                                  74 AsnlysGlulysGlnCysSerIleGluTrpSerAspGlySerSerIleSerLysGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 TGCCCAGAAGGCACCAATGCCTATCGCTCCTACTGCTACTATTAATGAAGACCGTGAG
                                  192 CTCACAGCAGTGAGAGCGATTGTGTNNNNNNNNNNTGGTCACGTTGACCACACC
                                                                                                                                                                                                                                                                                                       114 TrpGluAsnPheTyrCysGluGlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dieckgraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
FILE REFERENCE: 04255.75314
CURRENT APPLICATION UNBER: US/09/146,969
UUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
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444
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                    ----CGTGAACAATTTGAATGTCTC---
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09146969; Patent No. 6228585; GENERAL INFORMATION:
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53.03%
33.33%
28.18%
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Best Local Similarity:
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1356 AGCATCCACAGCATGGCTGAGCTGCAGTTCATCACCAAACAGATCAAGAGGAGGTGGAG 1415
                                     1429 AACTTCCGGGACAGTCTGGAGGACTGTGTCACCATCTGGGGCCCGGAAGGC-----CGC 1482
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                                                                                                               1483 TGGAACGACCCTGTAACCAGTCCTTGCCATCCATCTGCAAG 1527
                                                                                          114 TrpGluAsnPheTyrCysGluGlnGlnAspProPheValCysGlu 128
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Matches:
Conservative:
Mismatches:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-938-114-2 (1-129) x US-08-840-062-1 (1-4588)
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APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/840,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P1019R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                 Sequence 1, Application US/08840062
Patent No. 6117977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33,055
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4588 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197.50
52.59%
28.15%
27.62%
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EDNESS: Single
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-840-062-1
                                                                                                                                                                                       US-08-840-062-1
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                                                                                                                                                                  RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SerAlaLys1leHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrp---
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39
32
47
17
536 GTGCCTTGTGAAGACAAGTTCTCCTTTGTATGCAAG 571
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Matches:
Conservative:
Mismatches:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
FILING DATE:
FILING DATE:
FLING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-114-2 (1-129) x US-08-840-062-3 (1-4771)
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                                                                                                                             GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: WW. KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P1019R1
                                                                                          Sequence 3, Application US/08840062
Patent No. 6117977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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201.50
52.59%
28.89%
28.18%
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STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94080
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                                                                            US-08-840-062-3
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                                                        RESULT 5
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177 ATTGGCCTCCATGACCCCCAAAAGAACGCCCCCTGG-----CACTGGAGCAGTGGGTCC 230
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                                                                                                                                                                                           ----LysCys 102
                                                                                                                                                                                                                                                            103 LeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGluGlnGln 122
                                                                                                                                                                                                                                                                                                 291 GTGAGCCTGAAGCACAGGATTCCAGAAATGGAAGGATGTGCCTTGTGTAGACAAG 350
                                                                 .20 GGTGCCTTTGTGGCCTCACTGATTAAGGAGAGT---GGCACTGATGACTTCAATGTCTGG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Expression and Detection
                          48 AlaAspPhevalGlyGlnLeulleAlaGlnLysIleLysSerAlaLysIleHisValTrp
                                                                                                     68 ileçiyLeuArgAlaGlnAsnLysGluLysGlnCysSerIleGluTrpSerAspGlySer
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                                                                                                                                                                                 88 SerIleSerLysGluAsnTrp---IleGluGluGluSerLys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590
43
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49
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein C
TITLE OF INVENTION: of Alzheimer's Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [ndelB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lidwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                            123 AspProPheValCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                  351 TTCTCCTTTGTCTGCAAG 368
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~wormer: IBM PC compatible
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 590 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195.50
53.97%
34.13%
27.34%
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STRANDEDNESS: both
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                                                                               ----AATGATTTGAAACTGCAGATGAAT 1457
                                                                                                                                95 ---IleGluGluGluSerLysLysCysLeuGlyValHisIleGluThrGlyPheHisLys 113
                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
Annewserer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerTyrGluGlyHisCysTyrLysValPheLysGlnSerLysThrTrpThrAspAlaGlu 27
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3 GCCTATCGCTCCTACTGCTACTTTAATGAAGACCGTGAGACCTGGGGTTGATGCAGAT 62
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                                                                                                                                                                       1518 AACTITCGIGACAGCCIGGAGGACTGTCTCACCAICTGGGGGCCGGAAGGA
                                                                                                                                                                                                                                      114 TrpGluAsnPheTyrCysGluGlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590
43
25
49
                                                    81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INPORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2500
INFORMATION FOR SEQ ID No: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
-----GAGCTATGGATTGGCCTC-
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195.50
53.97%
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nucleic acid
EDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne,
STREET: 1100 New )
CITY: Washington
STATE: D.C.
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20005-3934
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US-08-454-557C-32
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                    1416
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Query Match: 27.34* Indels: 9 DB: 2 Gaps: 5	-09-938-114- 8	3 GCCTATCGCTCCTACTACTTTAATGAAGACCGGGAGACCTGGGTGAGATGAGATGAGATGATGATGATGATGATGATGA			Db 177 ATTGGCTCCATGACCCCAAAAGAACCGCCGCTGGCACTGGAGCAGTGCC 230 Qy 88 SerileSerLysGluAsnTrpIleGluGluGluSerLy8LysCys 102	231 CTGGTCTCCTACAGGCATTGGAGCCCCCAAGCAGTGTTAATCCTGGCTACTGT 103 LeuGlyValHislleGluThrGlyPheHisLySTrpGluAsnPheTyrCysGluGlnGln :::	Db 291 GTGAGCCTGACCAGGATTCCAGAATGGAAGGATGTGCTTGTGAAGACAAG 350 Qy 123 AsproPheValCysGlu 128	SULT 10 T-US95-17111 Sequence 32, GENERAL INF	ANT: Wands, Jack F DF INVENTION: Neur	OF SECTION OF SECTION NEW YOUR SETS.	; CTIY: Washington ; STATE: D.C. ; COUNTX: U.S.A. : ZIP: 20005-3934	23 5 5 6	11 12	ä	으러면 뭐	REFLEXENCE/DOCKET NUMBER: 36,203 REFREENCE/DOCKET NUMBER: 0609.3840002 TELEPONNUNICATION INFORMATION: TELEPONNE: (202) 371-2600 TELEPOND : (202) 371-2600	INFORMATION FOR SEQ ID NO: 32. SEQUENCE CHARACTERISTICS: LENGTH: 590 base pairs TYPE: nucleic acid STRANDEDNESS: both
	28 SerPheCysThrLysGlnValAsnGlyGlyHisLeuValSerIleGluSerSerGlyGlu ::: ::: :::	valrrp Grcree	Oy 68 IleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSerIleGluTrpSerAspGlySer 87	Qy 88 SerileSerLysGluAsnTrpIleGluGluGluSerLysLysCys 102	Qy 103 LeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGluGlnGln 122 ::::::	Oy 123 AspProPheValCysGlu 128 	RESULT 9 US-08-450-673C-32 ; Sequence 32, Application US/08450673C ; Patent No. 5948888 ; Patent No. 5948888	APPLICANT: de la Monte, Suzanne ; APPLICANT: Wands, Jack R. ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection ; TITLE OF INVENTION: of Alzheimer's Disease ; NUMBER OF SEQUENCES: 121	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Stearne, Kessler, Goldstein & Fox P.L.L.C. ; STREET: 1100 New York Avenue, Suite 600 ; CITY: Washington	; STATE: D.C. ; COUNTRY: U.S.A. ; ZIP: 20005-3934 ; COMPUTER READABLE FORM:	; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS	rerease #1.0, version #1.0 TA: US/08/450,673C -1995	; CLASSIFICATION: 530 ; ATTORNEY/AGENT INFORMATION: ; NAME: Ludwig, Steven R.	; REFERENCE/DOCKET NUMBER: 36,703 ; REFERENCE/DOCKET NUMBER: 0609.3840004 ; TELECOMMUNICATION INFORMATION: : TELEPHONE: (202) 371-2600	TAX: (202) 37 CON FOR SEQ ID TE CHARACTERIS TH: 590 base	; TYPE: nucleic acid ; STRANDEDNESS: both ; TOPOLOGY: both US-08-450-673C-32	Alignment Scores: 4.24e-16 Length: 590 Pred. No.: 195.50 Matches: 43 Score: 195.50 Matches: 43 Percent Similarity: 53.97% Conservative: 25 Best Local Similarity: 34.13% Mismatches: 49

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ZIP: 20004
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LOCATION:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 LeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGluGlnGln 122
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                                                                                                                                                                                               SerTyrGluGlyHisCysTyrLysValPheLysGlnSerLysThrTrpThrAspAlaGlu 27
                                                                                                                                                                                                                             3 GCCTATCGCTCCTACTACTACTTTAATGAAGACCGTGAGACCTGGGTTGATGCAGAT 62
                                                                                                                                                                                                                                                                                                                                                                                                        28 SerPheCysThrLysGlnValAsnGlyGlyHisLeuValSerIleGluSerSerGlyGlu
                                                                                                                                                                                                                                                                                                                         48 AlaAspPheValGlyGlnLeuIleAlaGlnLysIleLysSerAlaLysIleHisValTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: MUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
                                                         Length:
Matches:
Conservative:
                                                                                                                                                                  US-09-938-114-2 (1-129) x PCT-US95-17111A-32 (1-590)
                                                                                                      Mismatches:
Indels:
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08340428B
; Patent No. 5648465
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 TTCTCCTTTGTCTGCAAG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AspProPheValCysGlu 128
                                                         4.24e-16
195.50
53.97%
34.13%
27.34%
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                                                                                                        Best Local Similarity:
both
                                                                                        Percent Similarity:
   ;
PCT-US95-17111A-32
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TOPOLOGY:
                                           Alignment Scores:
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                                                                                                                     Query Match:
DB:
                                                             .. No. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSerIle 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuValSer 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 IleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLysSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
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APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULPATE PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3314 GGACACGAGAATTCATGGATTGGCCTGAATGACAGGACAGTAGAGAGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: |||| |||3275 GTCCACAGAAGACACAAGTTTTATTAACAGTTTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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            REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELECOMUNICATION INFORMATION:
TELEFAN: 202-628-5197
RELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5191 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application PC/TUS9307306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.39e-13
184.50
45.93%
28.89%
25.80%
Browdy, Roger L.
                                                                                                                                                                                                                                      STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            CDS
77..3847
                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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US-09-938-114-2 (1-129) x US-07-778-156-4 (1-522)
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                                                                                                                                                                                                                                                               COMPUTER FABDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
CLASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5436169man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
     IOVANNA, JUAN-LUCIO
KEIM, VOLKER
DAGORN, JEAN-CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 354
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.43e-14
183.00
48.89%
31.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: pancreas
                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unkno
MOLECULE TYPE: cl
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3314 GGACACGAGAATTCATGGATTGGCCTGAATGACAGGACAGTAGAGAGG-----GACTTC 3367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 ------SerLysLysCys---LeuGlyValHisIleGluThrGlyPheHisLys 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuValSer 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AlaLys1leHisValTrplleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSerlle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3275 GICCACTCCCCAGAAGAGCACAAGTITATIAACAGITIT------
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLING DATE: PCT/US93/07306
FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                  FILING DATE: 03-AUG-1933
FRIOM APPLICATION DATA:
APPLICATION NUMBER: US 07/922,911
FILING DATE: 03-AUG-1992
ATORNEY, AGENT INFORMATION:
NAME: TOWNERH, 34,033
REFERENCE/DOCKET NUMBER: Margolis=1A PCT
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x PCT-US93-07306-1 (1-5191)
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Matches:
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                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5191 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,39e-13
184.50
45.93%
28.89%
25.80%
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM
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77..3847
                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
PCT-US93-07306-1
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Pred. No.:
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US-07-778-156-4
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DB:
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352 GAAGGTTGGGAGTGGAGTAGCAGTGATGTGATGAATTACTTTGCATGGGAGAGAAATCCC 411
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APPLICANT: KEIM, VÖLKER
APPLICANT: DÄCORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
                                                                                                                                                            OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
                                                                                                                                                               STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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GENERAL INFORMATION:
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APPLICANT:
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---LysCysLeuGlyValHisIleGluThrGlyPheHisLys 113
                                              2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: INCOMINA,
APPLICANT: KEIM, VOLKER
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TOTAL OF INVENTION: PANCREATITIS
ADDRESSEE: 0BLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                114 TrpGluAsnPheTyrCysGluGlnGlnAspProPheValCysGlu 128
                                                                                                                                                                                         472 TGGAAAGATTATAACTGTAATGTGAGGTTACCCTATGTCTGCAAA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/422,166

FILING DATE: 14-APR-1995

CLASSIFICATION 1435

PRIOR APPLICATION NUMBER: US/07/778,156

FILING DATE: 19-DEC-1991

ATFORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION INFORMATION:

TELEFANCE/POCKET NUMBER: 354-012-0 PCT

TELEFANCE/POCKET NUMBER: 354-012-0 PCT

TELEFANCE/POCKET NUMBER: 354-012-0 PCT

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TELEFANCE/POCKET NUMBER: 354-012-0 PCT

TELEFANCE/POCKET NUMBER: 354-01
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Mismatches:
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Matches:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5959086
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: unknown
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TISSUE TYPE: pancreas
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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   SerLys--
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292 AGCTACTCATACGTCTGGATTGGGCTCCATGACCCCACACAGGCACCGAGGCCCAATGGA 351
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                                                                                    22 ThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuValSer 41
                                                                                                                                                                                                                                                                  42 IleGluSerSerGlyGluAlaAspPheValGlyGlnLeulleAlaGlnLysIleLysSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AlaLysIleHisValTrpileGlyLeuArg-----AlaGlnAsnLysGlnLysGlnCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 ---SerlleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGlu 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
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FR: 2121-107P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iovanna, Juan-Lucio
Dagorn, Jean-Charles
Keim, Volker
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NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 703-205-8000
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       SerLys-----LysCysLeuGlyValHisIleGluThrGlyPheHisLys 113
                                                                                                                                                                                                                                                                                                        42 IleGluSerSerGlyGluAlaAspPhevalGlyGlnLeuIleAlaGlnLysIleLysSer 61
                                                                                                                                                                                                                                                                                                                                                                                                      ---SerileGluTrpSerAspGlySerSerileSerLysGluAsnTrpIleGluGluGlu 98
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                                                                                                                                                                                                             2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "human
pancreatitis-associated protein"
/note= "see, Fig. 3"
                                                                                                      797
43
23
59
10
                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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FEATURE:

NAMEM KEY:

COCATION: 43..567

COTHER INFORMATION:

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US-08-464-637-1
                                                                                                                   Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Search completed: December Job time: 106.726 secs

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Sequence 10, Appl
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Sequence 11, Appl
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Sequence 3709, Ap
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Sequence 1759, Ap
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Sequence 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jin Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and
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13 US-09-997-003-11
3 US-09-997-003-11
3 US-09-997-003-1340
13 US-09-997-003-24
13 US-09-997-003-24
14 US-09-764-870-15
15 US-10-125-219-1734
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1.3 US-10-226-420-4

1.4 US-09-929-230-7

1.5 US-09-929-230-7

1.6 US-09-929-230-10

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1. US-09-929-230-10

3. US-10-226-420-9

4. US-09-929-230-12

3. US-10-226-420-12

4. US-09-969-765-2

1. US-09-969-765-2

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published_Applications_NA:*

Database

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Scoring table:

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LOCATION: (91)...(546)
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NAME/KEY: misc_feature
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LENGTH: 721
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Sequence 4, Application US/09929230

Patent No. US20020161203A1

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PRO
FILE REFERENCE: 00-72

CURRENT PAPLICATION NUMBER: US/09/929,230

CURRENT FILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-938-114-2 (1-129) x US-09-938-114-1 (1-544)
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,740
FILING DATE: «Unknown»
ATTORNEY, AGENT INFORMATION:
NAME: Chen, Anthony C.
REGISTRATION NUMBER: 38,673
REFERENCE, DOCKET NUMBER: 233/298
TELECHMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                            CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/938,114
FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                       LENGTH: 544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
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Sequence 4, Application US/10226420;
Bublication No. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS;
CURRENT APPLICATION NUMBER: US/10/226,420;
CURRENT FILING DATE: 2002-08-21;
NUMBER OF SEQ ID NOS: 14
SOSTWARE: FRASESEQ for Windows Version 4.0
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Mismatches:
Indels:
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Matches:
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                     SEQ ID NO 4
LENGTH: 721
TYPE: DNA
ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                  2.41e-57
477.00
76.74%
64.34%
                                                                                                                                                                               CTHER INFORMATION: Zsnk3
                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (91)...(546)
NAME/KEY: misc feature
LOCATION: (0)...(0)
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276 ACGAAGTGGAGCGATGCTCCAGCGTCAATTATGAGAACCTGATTAAACATGCGACGAAA 335
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                                                                        1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                             41 SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
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; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Paul 0.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; TITLE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 7
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; OTHER INFORMATION: Zsnk4
US-10-226-420-7
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NAME/KEY: CDS
LOCATION: (3)...(434)
FEATURE:
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Best Local Similarity:
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APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 580
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Patent No. US20020161203A1
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j OTHER INFORMATION: ZSDK3
US-10-226-420-4
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OTHER INFORMATION: ZBnk4
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NAME/KEY: misc_feature
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Best Local Similarity:
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Pred. No.:
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                                                                                                         81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
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                              SeralalysileHisValTrpileGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
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NAME/KRY: misc_feature
LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63,
LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 114, 117, 129, 135, 147, 153,
LOCATION: 66, 69, 78, 81, 84, 90, 93, 114, 117, 129, 135, 147, 153,
LOCATION: 22, 171, 177, 180, 186, 189, 192, 201, 204, 211, 216, 222,
LOCATION: 225, 231, 234, 237, 246, 249, 252, 255, 261, 276, 279
OTHER INFORMATION: n = A,T,C or G
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NAMBLKEY: misc_feature
LOCATION: 282, 285, 291, 309, 312, 321, 327, 330, 333, 336, 339, 360,
LOCATION: 366, 373, 381, 384, 393, 396, 414, 429, 441, 447, 456
OTHER INFORMATION: n = A,T,C or G
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ID NO:5.
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Mismatches:
Indels:
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; Sequence 6, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PRO; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: This degenerate nucleotide OTHER INFORMATION: amino acid sequence of SEQ
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Matches:
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Best Local Similarity:
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      SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys
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OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:5.

NAME/KEY: misc feature
LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, LOCATION: 66, 69, 78, 81, 84, 90, 93, 114, 117, 129, 135, 147, 153, LOCATION: 162, 171, 177, 180, 186, 189, 192, 201, 204, 213, 216, 222, LOCATION: 225, 231, 234, 237, 246, 249, 252, 255, 261, 276, 279
OTHER INFORMATION: n = A,T,C or G
LOCATION: 282, 291, 309, 312, 321, 327, 330, 333, 336, 339, 360, LOCATION: 366, 372, 378, 381, 384, 393, 396, 414, 429, 441, 447, 456
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72

CURRENT APPLICATION NUMBER: US/09/929,230

CURRENT FILING DATE: 2001-08-13

NUMBER: OF SEQ ID NOS: 14

SEQ ID NO 6

LENGTH: 456
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Matches:
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Patent No. US20020161203A1
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US-09-929-230-6
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                                                                                                                                                                 523 GAAAAAACCTTTTCGTCTGCAAG 546
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TYPE: DNA
ORGANISM: Sistrurus miliarius
PEATURE:
NAME/KEY: CDS
LOCATION: (88) ... (561)
FEATURE:
NAME/KEY: misc_feature
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US-10-226-420-10
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81 IleGluTipSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
                                                                                                                                                                                                                                                        101 LyscysieucjyvalHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
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US-09-929-230-10

Sequence 10, Application US/09929230

Sequence 10, Application US/09929230

Batent No. US-0020161203A1

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul D.

TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS

FILE REFERENCE: 00-72

CURRENT FILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGH#: 725

TYPE: DNA

ORGANISM: Sistrurus miliarius

NANAWANISM: Sistrurus miliarius
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US-09-929-230-10
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LOCATION: (88)...(561)
NAME/KEY: misc_feature
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Best Local Similarity:
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101 LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
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|TCTGTCGAAAACGATGAAGAAGAGTCTTTCTGGCCCAGTTGGTCGCTGCGAACATAAAG 342
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463 AAGIGITITGGGCTGAAAAAGAGACAGAGTITCTICAATGGTACAIACTGACTGCGAA
                                                                                                                                                               RESULT 9
US-10-226-420-10
Sequence 10, Application US/10226420
Sequence 10, Application US/10226420
Publication No. US20030127686A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: RATILESNAKE VENOM GLAND PROTEINS
FILE REFRENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 CARAAYAARTAYGAYGTNTGGATHGGNYTNMGNATHCARGGNGARGARAARCARTGYWSN 273
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                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: This degenerate nucleotide sequence encodes the CTHER INFORMATION: amino acid sequence of SEQ ID NO:8.

NAME/KEY: misc feature
LOCATION: f, 126, 135, 141, 144, 150, 153, 156, 165, 171, 171, 18
LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 18
LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 273, 273, 274, 274, 285, 273, 273, 273, 274, 274, 287, 330, 315, 327, 330, 345, 348, 360
CHER INFORMATION: n = A.T.C or G
LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
US-09-929-230-9
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Indels:
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                Sequence 9, Application US/09929230; Sequence 9, Application US/09929230; Patent No. US20020161203A1; GENERAL INFORMATION: APPLICANT: Sheppard, Paul O. APPLICANT: Bishop, Paul D.; TITLE OF INVENTION: RATILESNAKE VENOM GLAND; FILE REFERENCE: 00-72; CURRENT APPLICATION NUMBER: US/09/929,230; CURRENT FILING DATE: 2001-08-13; NUMBER OF SEQ ID NOS: 14; SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 99
                                                                                                                                   GLAND
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CARCARAAYYINTTYATGTGYAAR
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                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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378.00
62.50%
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Best Local Similarity:
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RESULT 10
US-09-929-230-9
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LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
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                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
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NAME/KRY: misc_feature

LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 10 CATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 10 CATION: 186, 199, 199, 198, 201, 231, 240, 243, 246, 255, 273, 10 CATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360 OTHER INFORMATION: n = A,T,C or G
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                                                          PROTEINS
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NAME/KEX: misc. feature
LOCATION: 363, 369, 372, 378, 384, 393, 405, 423,
OTHER INFORMATION: n = A,T,C or G
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Matches:
Conservative:
Mismatches:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PR(TILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-114-2 (1-129) x US-10-226-420-9 (1-432)
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                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity:
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196 WSNGTNGARAAYGAYGARGARGCNGTNTTYYTNGCNCARYTNGTNGCNGCNAAYATHAAR 255
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OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:11.

NAME/KEY: misc feature

LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, 10CATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, 10CATION: 168, 177, 183, 186, 192, 195, 198, 201, 219, 222, 228, 231, 10CATION: 237, 240, 243, 246, 273, 282, 285, 288, 303, 315, 318

NAME/KEY: misc feature

LOCATION: 327, 333, 336, 339, 342, 345, 357, 360, 366, 372, 387, 390, 10CATION: 327, 311, 426, 447, 453, 465, 468

US-09-929-230-12
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APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT PEPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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Publication No. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Pred. No.:
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136 AARACNTGGGAYGAYGCNGARMGNTTYTGYWSNGARCARGCNAARGGNGGNCAYYTNGCN 195
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                                                                                                                                                                            OTHER INFORMATION: This degenerate nucleotide sequence encodes the PEATURE:
PRATURE:
LOCATION: misc_feature
LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63, LOCATION: 6, 9, 84, 87, 90, 99, 120, 123, 132, 135, 141, 153, 159, LOCATION: 66, 69, 84, 87, 90, 99, 120, 123, 132, 135, 141, 153, 159, LOCATION: 168, 177, 183, 186, 192, 195, 198, 201, 219, 222, 228, 231, OTHER INFORMATION: n = A,T,C or G
FEATURE:
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LOCATION: 327, 333, 336, 339, 342, 345, 357, 360, 366, 372, 387, 390,
LOCATION: 402, 411, 426, 447, 453, 465, 468
OTHER INFORMATION: n = A,T,C or G
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
SOFTWARE: FASLSEQ ID NOS: 14
SOFTWARE: FASLSEQ for Windows Version 4.0
SEO ID NO 12
TYPE: DNA
TYPE: DNA
CREANISM: Arcificial Sequence
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APPLICANT: KITO, MORIKAZU
APPLICANT: KAYAHARA, TAKASHI
APPLICANT: FUTAKI, FUME
APPLICANT: ISHIKAWA, KOHKI
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                                                                                                                                                              FEATURE:
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101 LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 TATTGTACAGTAATGGTAGTCAAGACAGATAGGATCTTTTGGTTCAATAGAGGTTGCGAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                240 TTCACTTCC----ATGTGGATCGGACTGAAA-----GATCTATGGAAAGAATGCAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 SerileGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys 60
                                                                                                                                                                                                                                                                                                                                                         1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                  60 GATTGTCCCTCTGACTGGTCCTCCTATGATCAGCATTGCTACAAGGTCTTCAGTGAACTC
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 AAGACTGTATCTTTTGTCTGCAAG 425
                               TYPE: DNA ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                  1.48e-27
                                                                                                                                                                                                                           264.00
57.03%
42.97%
36.92%
                                                                FEATURE:

NAME/KEY: CDS

LOCATION: (3)...(455)

NAME/KEY: misc_feature

LOCATION: (0)...(0)

GOTHER INFORMATION: ZSHK2
US-09-929-230-1
                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
             LENGTH: 483
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 SEQ ID NO 1
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APPLICANT: SUZUKI, EIICHIRO
APPLICANT: GONDOH, KEIKO
APPLICANT: GONDOH, KEIKO
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: YAMADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING FILE REFERENCE: 214760USO
CURRENT FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: JP 2000-305279
PRIOR APPLICATION NUMBER: JP 2000-305279
PRIOR PILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LysCygLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyrCysGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 TACCTCACACGTTATATATCTGGATTGGACTGAGGGTTCAAAACAAAGGACAGCCATGC--- 377
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Patent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATILESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FageLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                     1.65e-30
286.50
60.16%
42.97%
40.07%
                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Crotalus harridus
                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS
; LOCATION: (66)..(512)
; OTHER INFORMATION:
US-09-969-763-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                LENGTH: 690
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483 18 18 6 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 8, 2003, 09:49:54; Search time 25.8 Seconds (without alignments) 480.843 Million cell updates/sec Run on:

US-09-938-114-2 Title: Perfect score: Sequence:

715 1 DCSSDWSSYEGHCYKVFKQS......GFHKWENFYCEQQDPFVCEA 129 Scoring table:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description		ayarsacutacili arbii	COAGLIACION FACTOR	botrocetin elekt	addretin alpha cha	hitiscetin alpha cha	Coadilation factor	addretin heta chai	adkisacutacin heta	bitiscetin heta ch		ק ק ק	Coadulation factor	Technical dalactore	redenerating islet	Dangreatic atone n	Droteoglycan core	addrecan - howine	۲,	lectin - Therian r	i e	red T. redeneration	red II redenarati	nroteogiscan core	addredan preduction	Aggreent Precuison	pancicucitie assoc	pancteatic untedu	pancicacilla-assoc
SUMM	ID	JC7134	JC4329	JC4690	A47267	PC7027	JC5058	JC4691	JC7105	JC7135	JC5059	B47267	JC2415	B42972	A38609	RGHU1A	A45751	A39808	T42630	T42710	S32489	RGHULB	A4714B	B47148	A28452	A55182	S54979	A37194	529822	552781
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	Length	152	129	152	133	144	131	146	146	146	125	125	123	123	135	166	166	1340	2327	1479	172	166	165	173	2124	2132	174	175	175	1268
æ	Query Match	95.8	73.7	69.4	59.1	58.8	48.3	40.7	39.5	38.3	37.9	36.4	35.2	34.7	32.4	28.2	28.2	27.9	27.9	27.6	27.1	26.9	26.6	26.5	26.5	26.5	26.1	26.0	26.0	25.9
	Score	685	527	496	422.5	420.5	345	291	280	274	271	260	252	248	231.5	201.5	201.5	199.5	199.5	197.5	194		190.5	189.5		189.5	186.5	186	186	
	Result No.	1	7	9	4	S	9	7	8	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Coagulation factor IX-binding protein A chain - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 13-Mar-1998
C;Accession: JC4229
R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A;Tile: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavoral A;Reference number: JC4329; MUID:96318509; PMID:8749314

RESULT 2 JC4329

redenerating prote	neurocan precursor	addredan predation	addredan bredar	Dangreatities	nancreatic atone n	Dance of the party of	hypothetical prote	phospholipase 10 r	Danchestic of a	phonetic acoust p	mannoso recentor r	secretors receptor p	secretory phosphol	TOR BO recentor]	chondroitin sulfat
183377	\$28764	150421	A39086	A49616	A28351	A48689	T29536	A49707	A41719	A53210	A36563	B56395	A56395	LINMSER	A47171
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174	1257	2109	2415	175	165	174	178	1458	175	1463	1456	1326	1465	331	3562
25.9	25.8	25.7	25.7	25.6	25.5	24.8	23.9	23.9	23.8	23.5	23.3	23.2	23.2	22.8	22.7
.185	184.5	183.5	183.5	183	182.5	177	171	171	170	168	166.5	166	166	163	162.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 JC7134	
agkisacutac N;Alternate	agkisacutacin alpha chain precursor - sharp-nosed viper N/Alternate names: fibrinogenlytic venom protesin
C;Species: C;Date: 04-	_ 6
C; Accession	JC7134, PC7037
	X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J. Biophys. Res. Commun. 265. 530-535. 1999
A; Title: Pu	Purification, characterization, and cDNA cloning of a new fibrinogenlytic
A; Accession: JC7134	A; Reterence number: UC/134; MUID:20025379; PMID:10558903 A; Accession: JC7134
A; Molecule type: mRNA	Lype: mRNA
A:Cross-ref	Ajkestudes; 1.152 < CKHE. Ajkosa-treferences GB-12176430
A; Experimen	A:Experimental source: venom gland
A; Accession: PC7037	: PC7037
A;Molecule t A:Residues:	A;Molecule type: protein A:Residues: 24-54.84-86.82-94.125.122-152
C; Superfami	C,Superfamily: tetranectin; C-type lectin homology
C; Keywords:	C; Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: sig F;24-152/Product:	F:1-23/Domain: signal sequence #status predicted <sig> F:24-152/Product: agkisacutacin alpha chain #status experimental <mat></mat></sig>
Query Match	
Best Local Matches 12	Similarity 96.1%; Pred. No. 6e-59; 24; Conservative 0; Mismatches 5;
δλ	LIAQKIK 60
Db du	24 DCSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK 83
δy	61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
qa	84 SAKIHUWIGLEAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCE 143
0, 13	121 QQDPFVCEA 129
Db 14	144 QQDFVCEA 152

venom

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botroccetin alpha chain - jararaca
NyAlternate names: two chain botrocetin alpha chain
NyAlternate names: two chain botrocetin alpha chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 2.1-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: A47267; B37958
B;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pun A;Reference number: A47267; MUID:93157385; PMID:8430107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Note: sequence extracted from NCBI backbone (NCBIP:124085)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sugi Biochemistry 30, 1957-1964, 1991
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally di A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: B37958
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C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 0.3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
R;Chung, C.H.; Au, L.C.; Huang, T.F.
R;Chung, C.H.; Au, L.C.; Huang, T.F.
A;Title: Molecular Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet
A;Reference number: PC7027; MUID:99443731; PMID:10512747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SA-KIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KSAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: protein
A, Molecule type: protein
C, Residues: 1-40 o FUJ>
C, Complex: heterodimer of alpha and beta (see PIR: B47267) chains
C, Superfamily: tetranectin; C-type lectin homology
C, Superfamily: tetranectin; heterodimer; venom
F, 2-128/ Domain: C-type lectin homology cLCH>
F, 2-128/ Domain: C-type lectin homology cLCH>
F, 2-128/ Domain: C-type lectin homology cLCH>
F, 2-12, 30-128/ 103-120/ Disulfide bonds: #status experimental
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es 35; Indels
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A;Residues: 1-144 <CHU>
A;Residues: 1-191 <CHU>
C;Superimental Bource: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom
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59.7%; Pred. No. 1.9e
iive 16; Mismatches
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Matches 77; Conservative
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A;Residues: 1-133 <USA>
A;Experimental source: venom
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A;Molecule type: protein
A;Residues: 1-129 <ATO>
C;Comment: This protein; C-type lectin homology
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; calcium binding; venom
F;2-127/Domain: C-type lectin homology <LCH>
F;2-137,102-119/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                     73.7%; Score 527; DB 2; Length 12 72.1%; Pred. No. 9e-44; tive 10; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                          93; Conservative
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number: A39332; MUID:91332000; PMID:1831197
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                                                      A; Molecule type: protein A; Residues: 24-146 <ATO>
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Ditiscetin alpha chain - puff adder
NiAlternate names: von Willebrand factor modulator protein
NiAlternate names: von Willebrand factor modulator protein
C;Species: Bitis arietans (puff adder)
C;Date: 31-Jan.1997 #sequence_revision 31-Jan.1997 #text_change 12-Feb-1999
C;Date: 31-Jan.1997 #sequence_revision 31-Jan.1997 #text_change 12-Feb-1999
R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz submitted to JIPID, January 1997
R;Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-131 «MAT»
A;Experimental source: snake venom
B;Mateui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modul
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Cispecies: Trimeresurus flavoviridis (habu)
Cistecies: Trimeresurus flavoviridis (habu)
Cistecies: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 20-Jun-2000
Cisteciesion: JC4661; B39332; JC4330
R;Macsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Richem. Biophys. Res. Commun. 220, 382-387, 1996
Airthe: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein
A;Reference number: JC4690; MUID:96184662; PMID:8645314
72 LADEDYVWIGLRAQNKEQQCSSEWSDGSSVSYENLIDLHTKKCGALEKLTGFRKWVNYYC 131
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A; Cross-references: DDBJ:DB3332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
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47.7%; Pred. No. 3.4e-26;
live 24; Mismatches 39; Indels
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                                                                                                                     132 EOMHAFVCK 140
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120 KNPFICKS 127
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RiAtoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A;Fille: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavo
A;Reference number: JC4329; MUID:96318509; PMID:8749314
A;Accession: JC4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggretin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Daces: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7105
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem: Biophys. Res. Commun. 263, 722-727, 1999
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Mccession: JC7105
A;Mccession: JC7105
A;Mclecule type: mRNA
A;Residues: 1-146 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 HSIF--WMGL--SNVWNQCNWQWSNAAMLRYKAWAEE--SYC--VYFKSTNNKWRSRACR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                   A.Wolecule type: protein
A.Residues: 24-146 <AT2>
C.Superfamily: tetranectin; C-type lectin homology
C.Keywords: anticoagulant; blood coagulation; lectin; venom
F.1-23/Domain: signal sequence #status predicted <SIG>
F.24-146/Product: factor IX/X binding protein chain B #status predicted <MAT>
F.25-142/Domain: C-type lectin homology <LGH>
F.25-36,53-142,119-134/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFQSSEEADFVVKLAFQTFG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-146 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agkisacutacin beta chain precursor - sharp-nosed viper N;Alternate names: fibrinogenlytic venom protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.7%; Score 291; DB 2;
46.1%; Pred. No. 6.3e-21;
tive 18; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.2%; Score 280; DB 2;
44.3%; Pred. No. 7.2e-20;
iive 18; Mismatches 41
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nes 59; Conservative 1
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Dotrocetin beta chain - jararaca
N;Alternate names: two chain botrocetin beta chain
N;Alternate names: two chain botrocetin beta chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
C;Accession: B47267; C37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad Sci. US.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pu A;Reference number: A47267; MUID:93157385; PMID:8430107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Note: sequence extracted from NCBI backbone (NCBIP:124086)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug biochemistry 30, 1957-1954, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally di A;Reference number: A37958; MUID:91129280; PMID:1993206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Mesidues: 1-123 < PENA
A; Residues: 1-123 < PENA
A; Residues: 1-123 < PENA
C; Comment: This protein inhibits agglutination of fixed platelets induced by several platibrand factor and alboaggregins.
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: anticoagulant; dimer
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C;Date: 2.1-Mar-1995 #sequence_revision 26-May-1995 #text_change 15-Oct-1996
C;Accession: JC2415
R;Peng, M.; Holt, J.C.; Niewiarowski, S.
R;Peng, M.; Holt, J.C.; Comunn. 205, 68-72, 1994
A;Title: Isolation, characterization and amino acid sequence of echicetin beta subunit, A;Reference number: JC2415; MUID:95091801; PMID:7999097
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   : ||||| : | : || : || : || : || --VLVWIGL--SHFWRICPLRWTDGARLDYRALSDEPI--CF---VAESFHNKWIQWTCN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%; Score 260; DB 2; 42.2%; Pred. No. 5.2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-125 <USA>
A;Experimental source: venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 QQDPFVCE 128
                                                                                                                          QODPFVCE 128
                                                                                                                                                                                                     RKKSFVCK 122
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                                                                                                                              121
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Matches
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C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: 07(7135; Per7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, S30-S35, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom A;Reference number: UC7134; MUID:20025379; PMID:10558903
A;Rocession: UC7135
A;Rocession: UC7134; MUID:20025379; PMID:10558903
A;Rocession: UC7135
A;Residues: 1-146 <URA
A;Residues: CF07038
A;Molecule type: protein
A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>
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A;Accession: UC5058
A;Reference number: UC5058
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-105 cMAr>
A;Residues: 1-105 cMAr>
A;Residues: 1-105 cMAr>
A;Reference number: UC5916
A;Reference number: UC5916
A;Reference number: UC5917
A;Residues: 1-125 cMAr>
A;Reference number: UC5917
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAr>
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A;Residues: 1-125 cMAr>
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A;Residues: 1-125 cMAr>
A;Residues: 1-125 cMAry
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C;Date: 31.Jan.1997 #sequence_revision 31.Jan.1997 #text_change 12.Feb-1999
C;Accession: JG5059, JG5917
R;Maceui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz submitted to JIPID, January 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 TDL--VWIGLK--NIWNGCYWKWSDGTKLDYKDW--REQFECL--VSRTVNNEWLSMDCG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFH-KWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SAKIHYWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DCPSEWSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: venom C; Comment: This protein is a modulator of a von Willebrand factor modulator. C; Superfamily: tetranectin; C-type lectin homology C; Superfamily: venom F; 4-121/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       itiscetin beta chain - puff adder
/Species: Bitis arietans (puff adder)
/Bate: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 125;
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41.4%; Pred. No. 4.5e-19;
tive 23; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.3%; Score 274; DB 2; Best Local Similarity 45.3%; Pred. No. 2.7e-19; Matches 58; Conservative 16; Mismatches 46
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les 53; Conservative
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A;Accession: S02767
A;Molecule type: protein
A;Residues: 23-47 <DEC>
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Matches 49; Conserv
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A;Molecule type: DNA
A;Residues: 1-166 <WAT>
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A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A nd A;Reference number: A42972; MUID:92332516; PMID:1629211
A;Goctents: V. r. siamensis
A;Accession: B42972
A;Accession: B42972
A;Accession: B42972
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A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Ac
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C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Dates: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 11-Aug-1995
C;Dates: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 11-Aug-1995
C;Hirabayashi, J.; Kusunoki, T.; Kasai, K.
J. Biol. Chem. 266, 2320-2326, 1991
A;Title: Complete primary structure of a galactose-specific lectin from the venom of A;Reference number: A38609; MUID:91115849; PMID:1989986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: B42972
                                                                                                                                                                                                                                                                                                                                                                                                                              61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MEL--VWIGL--SDYWRDCYWEWSDGAQLDYKAW--DNERHCFAA--KTTDNQWARRKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                      1 NCLPDWSVYEGYCYKVFKERMNWADAEKFCMKQVKDGHLVSFRNSKEVDFMISLAFPMLK
                                                                                                                                                                                                                                                                          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
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; Pred. No. 7.3e-17;
16; Mismatches 48; Indels
                                                                                                                           DB 2; Length 123
F;2-119/Domain: C-type lectin homology <LCH>F;2-13,30-119,96-111/Disulfide bonds: #status predicted
                                                                                                                   35.2%; Score 252; DB 2,
40.6%; Pred. No. 3e-17;
cive 18; Mismatches !
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                                                                                                                                                                                               52; Conservative
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A,Molecule type: protein
A,Residues: 1-135 <HIR>
                                                                                                                                                       Local Similarity
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Best Local Similarity
Matches 56; Conserv
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Figure ating islet lectin 1-alpha precursor [validated] - human
NyAlternate names: lithostathine; pancreatic thread protein (PPP); reg I protein; reg1-al
NyContains: pancreatic stone protein (PSP)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence revision 03-Aug-1995 #text_change 08-Dec-2000
C;Accession: ASIST; R2851; S12950; S02767; S02419; S00713; S01471; A25246
NyMatanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.
A;Title: Complete nucleotide sequence of human reg gene and its expression in normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: GB.JO5412
R.Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto, J. Biol. Chem. 263, 2111-12114, 1984
A.Fitcle: A novel gene activated in regenerating islets.
A.Reference number: A92704; MUID:88115343; PMID:2963000
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A; Residues: 1-166 <TER>
A; Cross-references: GB:MID:g190978; PIDN:AAA36558.1; PID:g190979
R; Itoh, T.; Tsuzuki, H.; Katoh, T.; Teraoka, H.; Matsumoto, K.; Yoshida, N.; Terazono, K
FERS Lett. 272, 85-88, 1990
A; Title: Isolation and characterization of human reg protein produced in Saccharomyces of
A; Reference number: S12950; MUID:91032149; PMID:2226837
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A;Title: Complete amino acid sequence of an immunoreactive form of human pancreatic stone A;Reference number: S00113; MUID:88029417; PMID:3665916
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A.Title: The disulfide bridges of the immunoreactive forms of human pancreatic stone prot A.Reference number: S02419, MUID:88152214; PMID:3345835
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                                                                                                                                                                        Length 135;
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C;Superfamily: tetranectin; C-type lectin homology F;3-131/Domain: C-type lectin homology <LCH>F;3-14,31-131,106-123/Disulfide bonds: #status predicted
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                                                                                                                                                                        DB 2;
                                                                                                                                                               32.4%; Score 231.5; DB 2 36.6%; Pred. No. 3.2e-15;
                                                                                                                                                                                                                                           21; Mismatches
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A,Residues: 63-72;125-139;150-157;160-166 <ROU>
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119 NDQVCESKDAFLCQ 132
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A, Molecule type: protein
A, Residues: 23-52;160-166 < ITO>
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A; Accession: S00113

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A, Map position: 2p12-2p12
A; Introns: 22/1; 61/3; 107/3; 145/1
C; Superfamily: tetranectin; C-type lectin homology
C; Superfamily: tetranectin; C-type lectin; pancreas; pyroglutamic acid
C; Superfamily: tetranectin; C-type lectin; pancreas; pyroglutamic acid
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-166/Product: regenerating islet lectin 1-alpha #status experimental <MAT>F;23-166/Product: pancreating islet lectin 1-alpha #status experimental <MAT>F;34-162/Domain: C-type lectin homology <LMH*
F;23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F;23/Modified site: carbohydrate (Thr) (covalent) #status experimental
F;33-34/Cleavage site: Arg-Ile (trypsin) #status experimental
F;33-34/Cleavage site: Arg-Ile (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 34-73, X', 75-87, 'R', 89-98 < MON>
C; Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like cleat
C; Comment: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the growth
C; Genetics:
                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 33-48 <RO2>
K;Montalto, G.; Bonicel, J.; Multigner, L.; Rovery, M.; Sarles, H.; De Caro, A.
Biochem. J. 238, 227-232, 1986
A;Title: Partial amino acid sequence of human pancreatic stone protein, a novel pancreat
A;Reference number: A25246; MUID:87099950; PMID:3541906
                                                                 Rikouimi, F.; Bonicel, J.; Rovery, M.; de Caro, A.
PERS Lett. 216, 195-199, 1987
A;Title: Cleavage of the Arg-Ile bond in the native polypeptide chain of human pancreati
A;Reference number: S01471; MUID:87219142; PMID:3108036
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Best Local Similarity 33.3%; Pred. No. 3.2e-12;
Matches 44; Conservative 26; Mismatches 53;
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Cross-references: GDB:132455; OMIM:167770
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A; Molecule type: protein A; Residues: 34-166 <DE1>
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Search completed: December 8, 2003, 09:55:34 Job time: 25.8 secs

152 VPČEDKFSFVČK 163

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2003, 09:46:14 ; Search time 16.9543 Seconds (without alignments) 357.812 Million cell updates/sec December Run on:

US-09-938-114-2 score: Perfect

1 DCSSDWSSYEGHCYKVFKQS......GFHKWENFYCEQQDPFVCEA 129 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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EMBL; D83331; BAA11887.1; -.

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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=96184662; PubMed=8645314;
Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
"CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom.";
Biochem. Biophys. Res. Commun. 220:382-387(1996).
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-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
-!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97331317; PubMed=187649;
Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
of C-type lectin domains."
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
                                                                    01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor IX/factor X-binding protein A chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Atoda H., Hyuga M., Morita T., "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis.
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protein, tetranectin, and lymphocyte Fc epsilon receptor for
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-!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
            152 AA.
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        PRT;
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MEDLINE=91332000; PubMed=1831197;
                                                                                                                                                                                                                                                                           Trimeresurus flavoviridis (Habu)
    STANDARD;
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                                                                         COAGULATION FACTOR IX/FACTOR X-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 1. Trimeresurus albolabris (White-lipped pit viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
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INTERCHAIN (WITH C-98 OF B CHAIN)
                                                                                                                                                                                                                                                                                       Length 152;
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                                                                                                                                                                                                                                                                                                      31; Indels
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                                                                                 PROTEIN A CHAIN.
C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                       69.4%; Score 496; DB 1; 67.4%; Pred. No. 2.8e-40;
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      InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PR0059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
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MEDLINE=98189535; PubMed=9531050;
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87; Conservative 1
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152 AA;
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Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
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15-SEP-2003 (Rel. 42, Last annotation update)
Botrocetin, alpha chain (Platelet coagglutinin).
Bothrops jararaca (Jararaca).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
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Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Calvete J.J., Niewiarowski S.; "Alboaggregins A and B. Structure and interaction with human platelets.";
                                                                                                                                --- FUNCTION: Binds to platelet GPID/IX receptor system and agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Indels
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BY SIMILARITY.
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BY SIMILARITY.
B3569F5BP91F6624 CRC64;
                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23806; 11XX.
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                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SWART; SMO034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                Thromb. Haemost. 79:609-613(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 AA; 15427 MW;
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TISSUE=Venom;
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P81115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIE-SSGEADFVGQLIAQKI 59
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-!- FUNCTION: Two-chain Botrocetin forms an activated complex with VF, and the complex then binds to platelet GPIb, resulting in platelet agglutination.
-!- FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain Botrocetin in promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                             Liddington R.C.;
"Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                           'WF binding to platelets.
-!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
WF and Botrocetin form a soluble complex.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
PIR; A47267; A47267.
PDB; IIJX; 17-JUL-02.
PDB; IFVU; 14-FEB-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alboaggregin A subunit 2.5 amolacion upuate;
Trimeresurus albolabris (White-lipped pit viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH C-75 IN BETA CHAIN)
              MBDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98189535; PubMed=9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.1%; Score 422.5; DB 1; Length 56.9%; Pred. No. 2.3e-33; live 20; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15215 MW; E4CF4502946AC74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AA.
CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CINT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                     InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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128
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                                                                     toxin botrocetin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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P81112;
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Thromb. Haemost. 79:609-613(1998).

Thromb. Haemost. 79:609-613(1998).

-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.

-!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.

-!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.

-!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.

-!- SIMCARITY: Contains 1 C-type lectin family domain.

HSP; P23806; IIXX.

INTERPRO; IRRO01304; Lectin_C.

BR Ffam; PF00059; lectin_c; 1.

SNART; SM0034; CLECT; 1.

PROSITE; PS0041; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 EKHYVMIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLGCIQ 123
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Thromb. Haemost. 79:609-613(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEBESKKCLGVHIETGFHKWENFYCEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin B alpha subunit.
Trimeresurus albolabris (White-lipped pit viper).
Trimeresurus Squamata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98189535; PubWed=9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Indels
                                      agglutination.
                                                                    disulfide-linked.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23806; 11XX.
InterPro; PRR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PR00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                      C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                5F9D71FC86DE2435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 408; DB 1;
56.7%; Pred. No. 5.4e-32;
tive 21; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AA.
                                                                                                                                                                                                                        SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                15556 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Conservative
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129
121
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124 LNPFVCK 130
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DOMAIN
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                                                                                                                                                                                                    61 XXXXYXXXIGLSVQNKXQQCSSEWSDGSSVTYENLIXXXXXXKCFVLKKESEFRTWSNVYCE 120
                                                                                                                                                                                        SAKIHVWIGIRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                           9
                                                                                                                                                          1 DCPSDWSSFKQYCYQIVKELKTWEDAEXFCSEQANDGHLVSIESYREAVFVAELLSENVX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 24-48; 61-68; 108-120; 139-145 AND
                                                                                                                                          1 DCSSDWSSYEGHCYKVFKQSKTWTDARSFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence Convolution alpha precursor (CVX alpha).
Crotalus durissus terrificus (South American rattlesnake).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalus.
Niberidae; Crotalus.
           BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-75 IN BETA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
aggregating protein from Cotalus durissus terrificus venom.";
Biochem. J. 333:389-393(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
-!- SUBUNIT: Heterohexamer of three alpha chains and three beta
chains; disulfide-linked.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                              Length 132;
                                                                                            ; Score 388; DB 1; Length 13:
; Pred. No. 4.2e-30;
21; Mismatches 40; Indels
                                                          BY SIMILARITY.
6FAE64820383F16F CRC64;
  C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pram; PR00059; Lectin_c; 1.
PRINTS; PR01504; PNCEATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONVULXIN ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                      15419 MW;
                                                                                              54.3%;
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                                                                                                                    67; Conservative
 129
13
127
79
                                                          119
                                                                                                                                                                                                                                        QQDPFVCE 128
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                                                                     132 AA;
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Best Local
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                                                                                                                                                                                                                                                                                               2 CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS
                                                                                                                                                                                                                                                                                                                                       27 CPSDWYYYDQHCYRIFNEEMNWEDAEWFCTKQAKGAHLVSIKSAKEADFVAWMVTQNIEE
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino acid sequence of the alpha subunit and computer modelling of
the alpha and beta subunits of echicetin from the venom of Echis
carinatus (saw-scaled viper).";
Biochem. J. 323:533-537(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peng M., In W., Beviglia L., Niewiarowski S., Kirby B.P.;
"Echicetin: a snake venom protein that inhibits binding of von
"Hilebrand factor and alboaggregins to platelet glycoprotein Ib.";
Blood 81:2321-2328(1993)
--- FUNCTION: Binds to platelet GPIb and inhibits platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97250657; PubMed=9163349;
Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Sagi M.S.A.,
Clemetson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Viperinae; Echls.
                                                             INTERCHAIN (WITH C-100 IN BETA CHAIN) (POTENTIAL).
                                                                                                          BY SIMILARITY.
INTERCHAIN (WITH C-26 IN BETA CHAIN)
                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                  Length 158;
                                                                                                                                                                                                                                                         42; Indels
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23806; 1IXX.
                                                                                                                                                                        18141 MW; 949F9C6D673E2318 CRC64;
                                                                                                                                                                                                               ; Score 364; DB 1;
; Pred. No. 9.6e-28;
18; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; Pr00059; lectin_c; l.
PRINTS; PR01504; PROREATITSAP.
SMART; SM0004; CLECT; l.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA
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C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                      (POTENTIAL)
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Echis carinatus (Saw-scaled viper)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=93244424; PubMed=8481512;
                                                                                                                                                                                                                  50.9%;
                                                                                                                                                                                                                                   Local Similarity 52.8
nes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
      153
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                                                                                                                                                                            158 AA;
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      34
27
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104
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AC P81017;
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                                                                                                            DISULFID
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123 AA;
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96
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                                                                                                                                                                                                                               ABA4 TRIAB
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DISULFID
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                                                                                                                                                                                                                                                            61 SAKI--HVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFY 118
                                                                                                                                                                   DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang R., Kini R.M., Chung M.C.M.;
"Rhodocetin, a novel platelet aggregation inhibitor from the venom of Calloselasma rhodostoma (Malayan pit viper): synergistic and noncovalent interaction between its subunits.";
Biochemistry 38:7584-7593(1999)
-!- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet.
-!- SUBUNIT: Hererodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by intersubunit displaced by i
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-!- MASS SPECTROMETRY: MW=15955.90; MW_ERR=1.44; METHOD=Electrospray.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                   INTERCHAIN (WITH C-75 IN BETA CHAIN)
                                                                                                                                           9
                                                                                                         Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 133;
                                                                                                                                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
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BY SIMILARITY.
N; 386EAC519DFC674D CRC64;
                                                                    8F11C2D0BDC70B16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                      Score 309; Db 1, No. 1.3e-22; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.2%; Score 302; DB 1
42.2%; Pred. No. 6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001304; Lectin_C.
Pfam; PR00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
SMOSITE; PS000615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                      ; Pred. No. 1.3e-
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA.
   BY SIMILARITY.
BY SIMILARITY.
                                                      SIMILARITY)
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                                                                    MW;
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                                                                                                      43.28;
                                                                                                                      Similarity 47.3%;
62; Conservative 2
                                                                    15803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodocetin alpha subunit.
                                                                                                                                                                                                                                                                                                                           || : |||:|
CEFKFPFVCKA 129
                                                                                                                                                                                                                                                                                                        119 CEQODPFVCEA 129
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
   127
119
81
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102 1
133 AA;
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                                                                                                Query Match
Best Local Similarity
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DISULFID
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                               DISULFID
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RHCA_AGKRH
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61 NKIYRSWIGLKIENKGQRSNLEWSDGSSISYENLYEPYMEKCFLMDHQSGLPKWHTADCE 120
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1 DCPDGWSSTKSYCYRPFKEKKTWEEAERFCTEQEKEAHLVSMENRLEAVFVDMVMENNFE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
                                             61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stimulates
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                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit at
Trimeresurus albolabris (White-lipped pit viper).
Trimeresurus albolabris (White-lipped pit viper).
The followantia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae, Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J., Calvete J.J., Niewiarowski S.; "Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelets.";
Thromb. Haemost, 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4, disulfide-linked.
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARIY: Contains 1 C-type lectin family domain.
HSSP; P23807; IIXX.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR002353; AntifreezeII.
PRINTS; PR00055; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D4CFBEE1219C9B1E CRC64:
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18; Mismatches 4
                                                                                                                                                                                                                                                                                                        123 AA
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                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                       121 QQDPFVCE 128
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RESULT 10

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47; Indels

27; Mismatches

Conservative

54;

Matches

Similarity

IXB TRIFL

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STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Struct. Biol. 4:438-441(1997).
-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH.A 1 TO 1 STOICHIOMETRY.
-!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97331317; PubMed=9187649;
Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
                                                                                                                                                                    MEDLINE=96184662; PubMed=8645314;
Mateuzaki R., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T.;
"CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
Protein from snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COAGULATION FACTOR IX/FACTOR X-BINDING
                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
                                                                                                                                                                                                                                                                           Atoda H., Hyuga M., Morita T.;
"The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.;
             P23807; Q91247;
01.NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 4b, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN B CHAIN.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-102 OF A CHAIN).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i-SUBCELLULAR LOCATION: Secreted.
-i- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 220:382-387(1996).
    146 AA
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PDB; 1BJ3; 16-MG-99.
INTERPRO; 1PR001304; Lectin_C.
Ffam; PF00059; 1ectin_c; 1.
SWART; SW00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                 MEDLINE=91332000; PubMed=1831197;
                                                                                      Trimeresurus flavoviridis (Habu)
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                                                                                                                                                                                                                                                                                                                                                                                                                       of C-type lectin domains.";
    STANDARD;
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142
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                                                                                                                                                                                                                                            SEQUENCE OF 24-146.
                                                                                                                                                          SEQUENCE FROM N.A.
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61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEBESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                                                                                                                            83
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
NCBI_TaxID=8747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-92 IN BETA CHAIN)
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                                                                                                                                                                                              Length 146;
                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                        16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                            40.7%; Score 291; DB 1;
46.1%; Pred. No. 7.4e-21;
iive 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB abounit.
Crotalus horridus horridus (Timber rattlesnake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0615; C_TYPE_LECTIN_1; FALSE_NEG
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       127 AA.
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                                                                                                                                                                                                                    59; Conservative
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 121 QODPFVCE 128
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                                                                                                                                                                                                        Local Similarity
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126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                        CROHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              ---LKWTNGASVSYENLYEPYIRKCFVVQPWEGKSKWYKADCEE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGF-HKWENFYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 T--FFWIG--ANNIWNKCNWQWSDGTKPEYKEWHEE--FECL---ISRTFDNQWLSAPCS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 CPSHWSSYDRYCYKVFKQEMTWADAEKFCTQQHTGSHLVSFHSTEEVDFVVKWTHQSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
                                                                                                                                                                                                                         Convulxin beta precursors (TXX beta).

Crotalus durissus terrificus (South American rattlesnake).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of sub., i, convoluxin, a collagen-like plateletaggregating protein from Crotalus durissus terrificus venom.";
Biochem. J. 333:389-393(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
-!- SUBUNIT: Heterohexamer of three alpha chains and three beta chains; disulfide-linked.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.9%; Score 264; DB 1; Length 148; 44.5%; Pred. No. 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
94D7E3E1BC693B9F CRC64;
                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                     148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONVULXIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1;
PROSITE; PS50041; C TYPE LECTIN 2;
                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 BY
17402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y16349; CAA76182.1; -. HSSP; P23807; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lectin; Glycoprotein; Signal.
            64 QRYRAWTGLTERN--
                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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145
26
                                         122 QDPFVCE 128
                                                                    118 KNAFLCK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
148 AA;
                                                                                                                                                                                                                                                                                                                                                                               Leduc M., Bon C.;
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                                                                                                                                                  CRODU
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DISULFID
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SEQUENCE
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                                                                                                                  RESULT
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                                                                                  2;
                                                                                                                                                                                   63 XLTRYIWIGLRVQNKGQPC-----SSIYSENLVDPFD--CPMVSRDTRLREWFKVDCE 113
                                                                                                                                                                61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                    1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                                                  ECPSGWSSYDRYCYKPFKOEMTWADAERFCSEQAKGRHLLSVETALEASFVDNVLYANKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodocecin beta embanic.
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Entranta: Matanna: Chordata: Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
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ن
                                                 DB 1; Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordara, Craniata, Vertebrata, Euteleost
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.6%; Score 269; DB 1; Length 129; 39.4%; Pred. No. 7.9e-19;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Indels
112 BY SIMILMANIA...
15162 MW; B5DA100D383E3547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                               45;
                                                              .9e-19;
                                                                                                                                                                                                                                                                                                                                                                                  15-UUL-1998 (Rel. 36, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Rhodocetin beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                       129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 7.9e-
23; Mismatches
                                              Score 273.5;
Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin_C.
                                                         41.48;
                                                                         53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
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15
115
                                                                                                                                                                                                                             121 QODPFVCE 128
                                                                                                                                                                                                                                                         114 OCHSFICK 121
            127 AA;
                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                    RHCB AGKRH
            SEQUENCE
DISULFID
                                          Query Match
                                                            Local
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RHCB_AGKRH
                                                                         Matches
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Best Local &
Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and chemical characterization of two structurally and functionally distinct forms of botrocetin, the platelet coagglutinin isolated from the venom of Bothrops jararaca.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vWP, and the complex then binds to platelet GPIb, resulting in platelet agglutination.

-!- FUNCTION: Two-chain Botrocetin forms or platelet GPIb, resulting in platelet agglutination.

-!- FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain Botrocetin in promoting vWF binding to platelets.

-!- SUBBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
                                                                                                                                                                                                                                                                                                              "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH C-80 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                   Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T., Fukui H., Sugimoto M., Ruggeri Z.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                             MEDLINE-93157385; PubMed-8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
PIR; B47267; B47267.
PDB; 11JK; 17-UJU-02.
PDB; 1FVU; 14-FEB-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15037 MW; 1ED2027ED817FCA0 CRC64;
                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-UTL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
20-trocetin, beta chain (Platelet coagglutinin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG. PROSITE; PS00615; C TYPE_LECTIN_2; 1. Lectin; 3D-structure.
                                                                                                        125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91129280; PubMed=1993206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_c; 1. SMART; SMO0034; CLECT; 1.
                                                                                                                                                                                                                                                       SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                Bothrops jararaca (Jararaca)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin botrocetin.";
Structure 10:943-950(2002).
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                   121 QODPFVCE 128
                                           138 DTYSFVČK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 AA;
                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 1-40.
                                                                                                                                                                                                                                                                                                       fitani K.;
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36.4%; Score 260; DB 1; Length 125;

Query Match

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MEDLINE=96420502; PubMed=8823201;
Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
Andrews R.K., Kroll M.H., Ward C.M.,
Andrews R.K., Kroll M.H., Ward C.M.,
Andrews R.K., Kroll M.H., Ward C.M.,
Andrews R.K., Kroll M.H., Ward C.M.,
Andrews R.K., Kroll M.H., Ward C.M.,
Andrews R.M.,
Brinding of a novel 50-kilodalton alboaggregin from Trimeresurus
T. Blodabris and related viper venom proteins to the platelet membrane
T. Glycoprotein Ib-mediated platelet activation.";
Blochemistry 35:12629-12839(1996).
T. FUNCTION: Blinds to platelet GPiBLIX receptor system, inhibits VWF
Dinding, and stimulates agglutination.
T. SIBUNIT: Hererodimer of alpha and beta subunits; disulfide-linked.
T. SIBUNIT: Hererodimer of alpha and beta subunits; disulfide-linked.
T. SIBURILALIAR LOCATION: Secreted.
T. SIMILARITY: Contains I C-type lectin family domain.
SNA00034; CLECT; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENW-IBEESKKCLGVHIETGFHKWENFYC 119
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                                                                                                                                                          61 SAKIHYWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
                                                                                                                                                                                             61 GDV.-VWIGL.-SDVWNKCRFEWTDGMEFDYDDYXLIAEYEC--VASKPTNNKWWIIPCT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                              1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
                                                                                                           1 DCPPDWSSYEGHCYRFFKEWMHWDDAEBFCTEQOTGAHLVSFQSKEEADFVRSLTSEMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels 14; Gaps
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHH-B beta subunit.

CHH-B beta subunit.

Crotalus horridus (Timber rattlesnake).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Crotalus.
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                      Indels
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07835BBCB61E9EAD CRC64;
                      51;
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42.2%; Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA.
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tes 52; Conservative 21; Mismatches
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117 AA;
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DOMAIN
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CHBB_CROHO
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Search completed: December 8, 2003, 09:53:09 Job time: 17.2876 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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ó 9 83 1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLLAQKIK 24 DCSSGWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK Gaps Yu H.-X., Xiang K.-J., Liu J., "cDNA sequencing and analysis of eleven C-type lectin-like protein Agkisacutacin A chain.

Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).

Bukaryota: Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi;

Lepidosauria: Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Deinagkistrodon. ; 0 Length 152; Indels subunits from Agkistrodon acutus.";
Chin. J. Biochem. Biophys. 0:0-0(2002).
EMBL; AR176420; AAF26286.2; -...
HSSP; P23806; 11XX.
InterPro; IPR001304; Lectin. C.
Ffam; PP00059; lectin. c; 1...
SMART; SM00034; CLECT; 1...
PROSITE; PS00015; C. TYPE LECTIN 1; 1...
PROSITE; PS50041; C. TYPE LECTIN 2; 1...
SEQUENCE 152 AA; 17109 MW; 76A0F636DBF0D7AB CRC64; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 98.0%; Score 701; DB 13; 98.4%; Pred. No. 2.6e-66; iive 0; Mismatches 2; Best Local Similarity 98.4 Matches 127; Conservative SEQUENCE FROM N.A. TISSUE=Venom Query Match

61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120

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61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGUHIETGFHKWENFYCE 120
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TISSUE-Venom gland;
TISSUE-Venom gland;
Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshimaru M., Chijiwa T.,
Chang C., Pukumaki Y., Ohno M.;
"Characterization and molecular evolution of an anticoagulant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046491; BAB21452.1; -.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databages. EMBL, AY091758; AAM22786.1; -. InterPro; IPR001304; Lectin_C. InterPro; IPR003990; Pangreatis_ac.
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Interpro; IPR03390; Pancreatis_ac.
Pfam; PF00059; lectin_C.
SPRANT; SR00034; CLECT; 1.
SPROSTE; PS00615; CTYPE LECTIN 1; 1.
SPROSTE; PS00615; CTYPE LECTIN 2; 1.
SROSTE; PS0041; CTYPE LECTIN 2; 1.
SEQUENCE 146 AA; 16461 MW; GADF0E032544316C CRC64;
                                                                                                                         Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS0041; C_TYPE_LECTIN 1; 1.
PROSITE; PS5041; C_TYPE_LECTIN 2; 1.
SEQUENCE 152 AA; 17108 MW; B0870F3DA0A4D23B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Factor XI/factor X binding protein A chain.
                                                                                                                                                                                                                                                                                                                                                 91.9%; Score 657; DB 13; 92.2%; Pred. No. 1.2e-61; cive 1; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Atches 119;
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Q98UJ0
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                SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCE 143
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Bukaryota; Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogawa T., Tani A.;
"Purification, Sequencing, and cDNA Cloning of a Heterodimeric Anticoagulant Protein from Agkistrodon actus Venom Gland."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB0368680; BAA99281.1; --
HSSP; P23806; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
91.9%; Score 657; DB 13; Length 152;
Best Local Similarity 92.2%; Pred. No. 1.2e-61;
Matches 119; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 POTENTIAL.
17124 MW; 5C59C0F503A4D223 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 0.1-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DRC-2001 (TrEMBLrel. 19, Last annotation update)
Anticoagulant protein A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu H., Xiang K., Wang Y., Liu J.; "A chain of ACF 1/2 from Deinagkistrodon acutus.";
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                                                                                                                                                                                                                                                                                                          152 AA
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Pfam; PR00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; pROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                        QODPFVCEA 129
                                                                                                                                                QODPFVCEA 152
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NCBI_TaxID=36307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=36307;
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147 RNPFVCEA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Fibrinogen clotting inhibitor A chain.
Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys brevicaudus).
                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                                                                         Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 66.4%; Score 475; DB 13; Length 152; Local Similarity 63.6%; Pred. No. 2.1e-42; les 82; Conservative 17; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
"A novel coagulation factor Xa inhibitor from Korean snake Agkistrodon halys) venom.",
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF190827; AAG17178.1; --
HSSP; P23806; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 23 POTENTIAL.
24 152 HALYXIN A-CHAIN.
152 AA; 17455 MW; BDD74DIDC280C28D CRC64;
                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PRINTS; PRO1504; PNREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                                                Halyxin A-chain precursor.
                                                                                                                                                        PRELIMINARY;
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121 QQDPFVCEA 129
                                           138 QONPFVCEA 146
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Matches
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Q9DG39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Kim D.S., Koh Y.S.;
"Purification and molecular cloning of snake venom fibrin clotting
inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
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                                                                                                                                                                                                                                                                                                                                                                                                     64.3%; Score 460; DB 13; Length 154; 60.2%; Pred. No. 8.1e-41; live 20; Mismatches 31; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 158;
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Y W. H., Xiang K., Liu J.;

L Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF463522; AAL66391.1; -.

R InterPro; IPRO01346; Lectin C.

R InterPro; IPRO0399; Pancreatis ac.

R Pfam; PF00059; lectin C; 1.

R PRINTS; PR00159; CLECT; 1.

SRART; SMART; SMO0034; CLECT; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

DR PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

SEQUENCE 158 AA; 17950 MW; Ā73A9CB95997BFD7 CRC64;
                                                                                   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF125309; AAD18055.1; -...
HSSP; P23806; 11XX.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PRAMI; SM0034; CLECT; L.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 154 AA; 17293 MW; BD06F7DDFA0D140D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.4%; Score 439; DB 13; Length 1
Best Local Similarity 60.2%; Pred. No. 1.4e.38;
Matches 77; Conservative 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OL-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Antithrombin 1 A chain.
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09 63

Gaps

1;

RESULT 8

OBAYAS OBAYAS

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61 SAKIHUWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SA-KIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 LADEDYVWIGIRAQNKEQQCSSEWSDGSSVSYENLIDLHTKKCGALEKLITGFRKWVNYC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 DCIPGWSAYDRYCYQAFSEPKWWEDAESFCREGVKTSHLVSIESSGEODFVAQLVAEKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TIEMBLrel. 22, Created)
01-OCT-2002 (TIEMBLrel. 22, Last sequence update)
01-OCT-2003 (TIEMBLrel. 23, Last annotation update)
C-OT-2003 (TIEMBLrel. 23, Last annotation update)
C-type lectin-like protein TMVA A chain.
Trimeresurus mucrosquamatus (Taiwan habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Protobothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelet aggregation activity from Trimeresurus mucrosquamatus
                                                                                                                                                                                                                                                                                                                                                                                                        58.8%; Score 420.5; DB 13; Length 136; 59.7%; Pred. No. 1e-36; tive 16; Mismatches 35; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  venom.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AAY099321; AAM43808.1; -.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                        Huang T.F.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 158 AA; 18101 MW; CD0B71F02289AA6E CRC64;
                                                                                                                                                                                                                                                                                                                                                 136 AA; 15796 MW; 3B474A4149F0027A CRC64;
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Pred. No. 8e-34;
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53.9%; Pred. No. 8e-34
tive 21; Mismatches
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                                                                                                                                        Pfam, PF00059; Lectin_C.
Pfam, PF00059; Lectin_c; 1.
SWART, SMORO34; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                EMBL; AF244900; AAF79952.1; -. HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Conservative
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                           Chung C.H., Au L.C.,
Submitted (MAR-2000)
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Best Local Similarity
IISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21542539; PubMed=11686327;
Wang W.J., Huang T.F.;
"A novel tetrameric venom protein, agglucetin from Agkistrodon acutus,
"A novel terrameric venom protein,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang W.-J., Ling Q.-D., Huang T.-F.;
"Molecular structure and functional characterization of agglucetin, a tetrameric glycoprotean ID-binding protein, from Formosan pit viper.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF540646, AAN23125.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Venom gland;
MEDLINE=99443731; PubMed=10512747;
Chung C.H., Au L.C., Huang T.F.;
"Molecular cloning and sequence analysis of aggretin, a collagen-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aggretin alpha chain (Fragment).
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglosa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea; Viperidae, Crotalinae, Deinagkistrodon.
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24 158 AGGLUCETIN-ALPHA 2 SUBUNIT.
158 AA; 17977 MW; 9D0A9C936ABEA5E4 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                      (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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Biochem. Biophys. Res. Commun. 263:723-727(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.4%; Score 439; DB 13; 60.2%; Pred. No. 1.4e-38;
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                                                                                                                                                                                                                                                 Agglucetin-alpha 2 subunit precursor.
                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acts as a glycoprotein Ib agonist."
Thromb. Haemost. 86:1077-1086 (2001)
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                                                                                               PRELIMINARY;
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146 QLNPFVCK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=36307;
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                                                                                                                                                             01-MAR-2003
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                                                                                               Q8AYA5
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Matches

셤 ò 엄 à g RESULT 9

091841

Gaps

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Gaps

2;

Length 131; Indels

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61 KSHSIDFVWIGLTYKGRWKQCSSEWSDGSKIKYQKWGKQQPRKCLGLEKQTEFRKWVNLY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 APNIGKSKYYWIGLRIENKKQQCSSKWSDYSSVSYENLVRGNVKKCPALEKKQGFRKWV 124
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                                                                                                                                                                                                                                                KSAKI-HVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Platelet glycoprotein IB-binding protein alpha subunit, GPIB-BP alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DCSSDWSSYEGHCYKVFKQSKTWT----DAESFCTKQVNGGHLVSIESSGEADFVGQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96209990; PubMed=8631868; Awasaki T., Fujimura Y., Usami Y., Suzuki M., Miura S., Sakurai Y., Awasaki T., Fujimura Y., Usami Y., Suzuki M., Miura S., Sakurai Y., Tamiuchi Y., Hirano K., Titani K.; Tomplete amino acid sequence and identification of the platelet glycoprotein Ib-binding site of jararaca GPIb-BP, a snake venom protein isolated from Bothrops jararaca."; protein isolated from Bothrops jararaca."; Protein isolated from Bothrops jararaca."; RSP: P23866; 11XX.

InterPro: IPR001304; Lectin_C.

RR PEam; PR00059; lectin_C: 1.

RR PEam; P800059; lectin_C: 1.

RR PEAM; SM0034; CIECT; 1.

RR PEAM; CIYPE_LECTIN 1; 1.

RR PROSITE; PS00615; C TYPE_LECTIN 1; 1.

RR PROSITE; PS00615; C TYPE_LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops jararaca (Jararaca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Epidosauria, Squamata, Scleroglossa; Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.5%; Score 382.5; DB 13; Length
51.1%; Pred. No. 1.2e-32;
ive 23; Mismatches 37; Indels
                           Interpro, IPR001304; Lectin C.
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
SEQUENCE 131 AA; 15439 MW; B95E6C5CBF317E24 CRC64;
                                                                                                                                                            DB 13;
                                                                                                                                                                            1.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 AA.
                                                                                                                                                        54.5%; Score 390; DB
54.6%; Pred. No. 1.7e
ive 17; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
Biochemistry 35:5264-5271(1996).
                                                                                                                                                   Query Match 54.5%;
Best Local Similarity 54.6%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    119 CEQODPFVCE 128
                                                                                                                                                                                                                                                                                                                                                                                                       121 ČEEPQRFTČE 130
              HSSP; P23806; 11XX
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Q9PSM6
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                                                                                                                                                                                                                                                                                                                                                                                          Shin Y., Okuyama I., Hasegawa J., Morita T.;
"Molecular cloning of glycoprotein Ib-binding protein, flavocetin-A,
which inhibits platelet aggregation.";
Thromb. Res. 99:239-247(2000).
                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
ECLV IX/X-BP alpha SUBUNIT=COAGULATION factor IX/factor X-binding
protein alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Echis.
NCBI_TaxID=40353;
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Chen Y.L., Tsai I.H.;
"Functional and sequence characterization of coagulation factor
IX/factor X-binding protein from the venom of Echis carinatus
leucogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 391; DB 13; Length 1
53.9%; Pred. No. 1.7e-33;
cive 21; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shin Y., Okuyama I., Hasegawa J., Morita T.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1341; AAN /2438.1; -.
158 AA; 18073 MW; 8C138650665CA454 CRC64;
                                                                                                                                                        O.-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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TISSUE-Venom gland;
MEDLINE=20402624; PubMed=10942790;
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                                                                                                                                                                                                                 Flavocetin-A alpha chain.
Trimeresurus flavoviridis (Habu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY149341; AAN72438.1;
SEQUENCE 158 AA: 18073 MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Conservative
                                                                                                                              PRELIMINARY;
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       121 QQDPFVCE 128
                                        146 RENPFVCK 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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DB 13; Length 142;

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PROSITE; 1 PROSITE; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 DCLPGWSCYIRPCYQPPKLLKTWEDAERFCTEQANGGHLVSFESAGEADFVAGVLSENIK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60
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                                                                                                                                                                                                                                                                                                                                                        Agkietrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

'H, Xiang K., Wang Y., Liu J.;

'A chain of antithrombin A from Deinagkistrodon acutus.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.2%; Score 380.5; DB 13; Length Best Local Similarity 54.7%; Pred. No. 2.1e-32; Matches 70; Conservative 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY091762; AAM22790.1; -...
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001309; Pancreatis_ac.
Pfam; PF00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00041; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
SEQUENCE 155 AA; 17715 MW; 66E55C95E997A1D7 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
494-Micetin alpha subunit precursor.
GPIBAL.
                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Antithrombin A A-chain.
Agkistrodon acceptation of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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Q9DEA2
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DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

KW Signal
FT SIGNAL
SIGNAL
SIGNAL
SQUENCE 155 AA; 17798 MM; 92840281A797AACD CRC64;

QUELY MATCH
SCAL Similarity 54.7%; Pred. NO. 4.3e-32; Indels 1; Gaps 1;

MATCHES 70; CONSELVATIVE 18; Mismatches 39; Indels 1; Gaps 1;

QY 1 DCSSDWSSYEGHCYKVFKOSKIWTDAESFCTKQNNGGHLVSIESSGEADFVGQLIAQKIK 60

QY 1 DCSSDWSSYIRFCYQPFKLLKTWEDAEFFCTEQANGGHLVSFESAREADFVAGULSENIK 83

QY 61 SAKTHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCFVLKKDTGFRTWENFYCE 120

QY 121 QQDPFVCE 128
Db 143 LKHVFMCK 150

Search Completed: December 8, 2003, 09:54:48
JOb time: 64.6571 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

8, 2003, 13:34:19; Search time 3342.94 Seconds (without alignments) 937.879 Million cell updates/sec 1 DCSSDWSSYEGHCYKVFKQS......GFHKWENFYCEQQDPFVCEA 129 US-09-938-114-2 December BLOSUM62 Scoring table: Perfect score: Sequence: Run on:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

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-UNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humand.0.cdi -LISST=45
-UNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humand.0.cdi -LISST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6

EST: * Database :

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em_estmu:*
em_estov:*
em_estpl:* em_esthum:* em_estro:* em_htc:* em estba:*

gb_est1:*
gb_htc:*
gb_est3:*
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gb_est6:*
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em_est6nn:*

em gas hum:* em_gss_inv:* em_gss_pln:*

em gss fun: *
em gss mam: *
em gss mus: * em gss

em_gss_pro:*
em_gss_rod:*
em_gss_phg:*
em_gss_vrl:*
gb_gssl:*

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | 01668 JL2H08F | 01648 JI.2BO3F | 01460 THIDDGE | OLERO DHOLOFI C | 01641 TITHOFF | 71631 JE11F | 71598 THAP11P | TITIENT SECTO | 97005:II. 69310 | 71459 JEZGUGE | 71653 JI.2D01F

 | 11683 PH012R S | 01637 JL1G11F | 559 JL2F01F | 01401 GH025F
 | 1417 GH061F | 1607 JH4H10F | 667 JL2H07F | 35 JH2B09F | SZ JHSELZF | 36 FHUISFB | 625 TLIENSE
 | 621 JL1D02F | 01618 JL1C07F | 01620 JLICILF | 1469 JH1E09F. | 01665 JL2H01F | 3095 ir53d01. | 2255 io93g12. | 654 JL2D07F | 320 JHZGUZF
 | 139 ilastra. | 158 id78a11 | 380 ip28a05
 | 359 im45h03 | 964 iq69f02 | 5597 io87q10
 | 74835 ip13b07 | 58012 ir76d01 | 78069 il40
 | 72731 io84b10. | 13297 ig82d01. | 209 ig80h07. |
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 | 3 BQ77643 | 2 BM31245 | 4 CA84208
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 | 4 CA77483 | 4 CA86801 | 3 BQ77806
 | 4 CA77273 | Z BM31329 | 2 BM31320 |
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 | 3.7 461 | 2.0 440 | 2.0 456 | 9.0 654
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 | 1.3 475 | 1.2 378 | 378 | 3.7.
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ALIGNMENTS

BM401668 RESULT 1

BM401668 556 bp mRNA linear EST 01-MAY-2002 JL2H08F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5, similar to Snake venom C-type lectin, mRNA sequence. BM401668 BM401668 DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE

BM401668.1 GI:20376296
EST.
Bothrops insularis (island jararaca)
Bothrops insularis
Buthrops incularis
Buthrops incularis
Cutazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

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116 AsnPheTyrCysGluGlnGlnAspProPheValCysGlu 128
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                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                        DEFINITION
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AUTHORS
TITLE
                                                                                                                                                                              ACCESSION
                                                                                 RESULT 2
BM401648
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                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="venom glands"
/close_lib="Stanke Bothrops insularis library IL3"
/close_lib="Stanke Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEMILIZ+; Site_l: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with Oilgo-(dr) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMILIZ+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGluGluSerLysLysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGlu 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 gereceaacaragogaaarecaaaracrargreregaregaacraagarraaacaaa 321
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                           Junqueira de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTB)
Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                  Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hople@@usp.br
This EST corresponds to cluster BITLOTA (see Reference)
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Matches:
Conservative:
Mismatches:
Indels:
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/db xref="taxon:8723"
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Location/Qualifiers
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51.13%
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             (bases 1 to 556)
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1 (bases 1 to 501)

3 unqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
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Contact: Paulo Lee Ho
Contror de Botecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Pax: 55 11 37 26 1505
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This EST corresponds to cluster BITL07A (see Reference)
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67
22
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Conservative:
Mismatches:
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Matches:
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EM401682 618 bp mRNA linear EST 01-MAY-2002 PH012F Snake Bothrops insularis library IL2 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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/clone_lib="snake Bothrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEM1LZf+; Site 1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
                                                                                                                                                                                                                                                     33 AGACCCCAATCCCATGTCTGGATCGGACTGAGGGTGGAGACACAAAGGACAGCAATGCAGC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 IleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIleGluGluGluSerLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 TCGAACTGGAGCGATGGCTCCTGCGTTATGAGAACCTGGTTGAACGAAGAACGAAA 442
                                                                                                                                                                                                                           1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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1 (bases 1 to 618)

1 (bases 1 to 618)

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                                                                                                                                                                                                                                      21 LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
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                460
61
15
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                                                                 Conservative:
Mismatches:
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                                             Matches:
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                     Length:
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                         Gaps:
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/db_xref="taxon:8723"
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Gene 299 (1-2), 279-291 (2002)
22347338
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59.80%
50.21%
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Best Local Similarity:
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Alignment Scores:
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/mol_type="mRNA"
/mol_type="mRNA"
/do_xref="taxon:8723"
/tissue type="venon:8723"
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                                                264 GCTCCGAACATAGGGAAATCCAAATACTATGTCTGGATCGGACTGAGGATTGAAAAGAAA 323
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              GlyGlyHisLeuValSerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIle 55
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
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1 Unquelizarde-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of Gene 299 (1-2), 279-291 (2002)
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460 bp mRNA linear EST 01-MAY-2
JH1D06F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                       AlaGlnLysileLysSerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLys
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Pax: 55 11 37 26 1505
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Location/Qualifiers
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venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The CDNAS were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pSRMILIE; vector (Promega). ESTS were generated from random clones and grouped in unique sequences. The putative identification of each EST or
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1 (Dasse 1 to 458)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTE)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                           cluster was obtained through Blast searches (e-value < e-05)."
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144 GAGAGCTGGGATGATGTGAGCTGGTATGATGCANANAGGTTCTGCTCGGAGCGAAG 203
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                                                                Paulo SP, BRAZIL, 05503-900
                                                                                                                                                              Email: hoplee@usp.br
This EST corresponds to cluster BITL07A (see Reference)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 others
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Matches:
Conservative:
Mismatches:
Indels:
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Centro de Biotecnología
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paul
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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BM401631
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DEFINITION
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Tue Dec

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/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEMIJZF+; Site_l: Eco Ri, Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Choning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally clone in pGEMILZF+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
                                                                                                                                                                                                                                                                                                                 BM401598 406 bp mRNA linear BST 01-MAY-2002 JH4F11F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                            96 GluGluGluSerLysLysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGlu 115
                                                                                                                            448 CGAGGAAATGTGAAAAAGTGTTTTGCGCTGGAAAAAAGAGAATGTTCNTAAGTGGTC 507
         GluLysGlnCysSerIleGluTrpSerAspGlySerSerIleSerLysGluAsnTrpIle 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidea; Crotalinae; Bothrops.

1 (bases 1 to 406)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
                                                    388 AAACANCAATGCAGCTCGAAGTGGAGCGATTACTCCAGCGTCAGTTATGAGAACCTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:8723"
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Bothrops insularis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hoplee@usp.br
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Best Local Similarity:
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ORIGIN
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TITLE
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MEDLINE
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COMMENT
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KEYWORDS
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                                                                                                   Eukaryota, Metazza, Chordata, Craniata, Vertebrata, Euteleostomi, Eupidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Bothrops.

1 (bases 1 to 511)

1 (bases 1 to 511)

A unqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of Gene 299 (1-2), 279-291 (2002)
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208 GAGAGCTGGGATGATGTGAGGTATGATGCAGAGAGTTCTGCTCGGAGCGGAGCGAAG 267
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                                                                                                                                                                                                                                                                                                                                             Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
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/organism="Bothrops insularis"
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                                                             Bothrops insularis (island jararaca)
Bothrops insularis
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/db_xref="taxon:8723"
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                    BM401631.1 GI:20376259
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ACCESSION
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TITLE
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Alignment Scores:
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/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Granke Bothrops insularis library IL3"
/clone_lib="Granke Bothrops insularis library IL3"
/clone_lib="Gran." venom glands, vector: pGEMILIE+; Site_l: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILIE+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putarive identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 01-MAY-2002
                                                                                                                                                                                                                                                                                249 TCTATCGAAAGCGCCGGAGAAGCAGACTTTGTGGCCCAGCTGGTCACTGAGAACATACAG 308
                                                       129 GATTGTAACCCTTATTGGTCCTCCTATGAAGGCGTTCCTACAGGTTCTTCAAAACACCG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota incuraca, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota incuraca, Colubrodesa, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotablinae, Bothrops.

1 (Dases 1 to 410)
Junqueira-de-Azevedo, I. L. M. and Ho, P. L.
A survey of gene expression and diversity in the venom glands of the pittviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                        80
                  1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                40
                                                                                                                                                                          SerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIleAlaGlnLysIleLys 60
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410 bp mRNA linear EST 01-MAY-2
JM4H07F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
BM401605
                                                                                                                                                                                                                                                          SerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLysGluLysGlnCysSer
                                                                                                  LysThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuVal
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL07A (see Reference)
                                                                                                                                                                                                                                                                                                                                  /organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
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Bothrops insularis
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JL2G06F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                    84 GAGTGTCCTCTGATTGGTCCACCATAGACAGTATTGCTACAAGTTCTTCCAACAAAG 143
                                                                                                                                                                                                                                                                                                                                                                                144 GAGAGCTGGGATGATGATGCTGGTATGCAGAGAGGTTCTGCTCGGAGCAGGCGAAG 203
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J. (bases I to 418)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
                                                                                                                                                                                                                                                                                                                                        21 LysThrTrpThr-----AspAlaGluSerPheCysThrLysGlnValAsn 35
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/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11Zf+; Site_1:
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
                                                                                                                                                                                                                                 1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                      36 GlyGlyHisLeuValSerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIle
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This BST corresponds to cluster BITL07A (see Reference)
Seg primer: M13F.
410
59
18
26
5
Length:
Matches:
Conservative:
Mismatches:
Indels:

    .418
    /organism="Bothrops insularis"

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Bothrops insularis
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/db_xref="taxon:8723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GluGluGluSerLysLysCysLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 CGAGGAAATGTGAAAAAGTGTTTG 407
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Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                 US-09-938-114-2 (1-129) x BM401605 (1-410)
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Centro de Biotecnologia
Instituto Butantan
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     58e-27
                          324.50
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54.63%
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venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The CDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGRMI1Zt vector (Promega). ESTS were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
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JH1D05F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Lepidosauxia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 440)
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A survey of gene expression and diversity in the venom glands of the pitruiper snake Bothrops insularis through the generation of expressed sequence tags (BSTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ThrTrpThrAspAlaGluSerPheCysThrLysGlnValAsnGlyGlyHisLeuValSer
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
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/Mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="wenom glands"
/tissue_type="wenom glands" library IL3"
/clone_lib="snake Bothrops insularis library IL3"
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/clone lib="snake Bothrops insularis library IL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AlaGlnLysIleLysSerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsnLys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLysGlnCysSerIleGluTrpSerAspGlySerSerIleSerLysGluAsn-TrpIl 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AspAlaGluSerPheCysThrLysGlnValAsn 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGlyHisLeuValSerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeuIle 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST.

Bothrops insularis (island jararaca)

Bothrops insularis

Bothrops insularis

Bothrops contagona, Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM401653 453 bp mRNA linear BST 01-MAY-2
JL2D01F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
Fax: 55 11 37 26 1505
Email: hopte@wusp.br
This BST corresponds to cluster BITL07A (see Reference)
Seg primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440
178
17
17
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
                                                                                                                                   organism="Bothrops insularis"
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                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:20376281
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312.50
72.82$
56.31$
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96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-05).
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BM401653.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
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                                                BM401683 461 bp mRNA linear EST 01-MAY-2002 PH012R Snake Bothrops insularis library IL2 Bothrops insularis cDNA 3' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

Viperidae; Crotalinae; Bothrops.

Junquelra-de-Azevedo, L.M. and Ho, P.L.
A Burvey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 LysGluLysGlnCysSerIleGluTrpSerAspGlySerSerIleSerLysGluAsnTrp 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 IleAlaGlnLysIleLysSerAlaLysIleHisValTrpIleGlyLeuArgAlaGlnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL09A (see Reference)
Seq primer: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               others
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57
13
23
1
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Mismatches:
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Matches:
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Bothrops insularis
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                                                                                                                                       BM401683.1 GI:20376311
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74.47%
60.64%
43.71%
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Best Local Similarity:
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Contact: I
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DB:
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                                                                     DEFINITION
                                                                                                                                                                              SOURCE
ORGANISM
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MEDLINE
PUBMED
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TITLE
                                                                                                                   ACCESSION
                                                                                                                                     VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="venom glands"
/tissue type="venom glands"
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/clone lib="Snake Bothrops insularis library II3"
/note="Organ: venom glands, Vector: pGEMIIZF+; Site_1: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTeChnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMIIZF+ vector (Promega). BSTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 GGCGGCCATCTGGTCTCTATCGAAAGCGATGAAGAAGCAGACTTTGTGGCCCCAGCTGGTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 AAACAGCAATGCAGCTCGAAGTGGAGCGATTACTCCAGCGTCAGTTATGAGAACCTGGTT 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GluLysGlnCysSerlleGluTrpSerAspGlySerSerlleSerLysGluAsn-TrpIl 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysThrTrpThr------AspAlaGluSerPheCysThrLysGlnValAsn 35
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1 (bases 1 to 453)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cluster was obtained through Blast searches (e-value <
                                                                                                                                                                          Contact: Paulo Lee Ho
Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto abrata.
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 1505
Email: hople@cusp.br
This BST corresponds to cluster BITL07A (see Reference)
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58
17
22
6
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bothrops insularis"
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312.50
72.82%
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Best Local Similarity:
                                                                                                                                                               12459276
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DB:
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No
                                                                                                                 JOURNAL
MEDLINE
PUBMED
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TITLE
                 REFERENCE
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22

DEFINITION

RESULT 13

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

MEDLINE PUBMED

COMMENT

JOURNAL

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/tiskue type="venom glands"
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/clone lib="soake Bochrops insularis shote="venom glands, Vector: pcEM112f+; Site 1: Eco RI; Site 2: Not I; Sug of memory from Bothrops insularis venom glands were primed with oligo-(dr) and reverse transcribed to conva using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM112f+ vector (Promega). ESTs were generated from random clones and grouped in unique
                                                                                             205 GAGAGCTGGGATGATGTGAGCTGGTATGATGCAGAGGGTTCTGCTCGGAGGAGGCGAAG 264
145 GAGTGTCCCTCTGATTGGTCCACCCATAGACAGTATTGCTACAAGTTCTTCCAAAAAG 204
                                                                                                                                                                                               265 GGCGGCCATCTGGTCTCTATCGAAAGCGATGAAGAAAGCAGACTTTGTGGCCCAGCTGGTC 324
                                                                                                                                                                                                                                                                                     21 LysThrTrpThr------AspAlaGluSerPheCysThrLysGlnValAsn 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidea; Crotalinae; Bothrops.

1 (bases 1 to 456)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM401659
JL2F01F Snake Bothrops insularis library LL3 Bothrops insularis cDNA 5, similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                               36 GlyGlyHisLeuValSerIleGluSerSerGlyGluAlaAspPheValGlyGlnLeulle
                                                                                                                                                                                                                                                     56 AlaGlnLysileLysSerAlaLysileHisValTrpileGlyLeuArgAlaGlnAsnLys
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                                                                                                                                                                                                                                                                                                                                                                                                       385 AAACAGCAATGCAGCTCGAAGTGGAGCGATTACTCCNGCGTCAGTTATGAGAAC 438
                                                                                                                                                                                                                                                                                                                                                          76 GluLysglnCysSerIleGluTrpSerAspGlySerSerIleSerLysGluAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1550, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL07A (see Reference)
Seq primer: M13F.
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Bothrops insularis
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AUTHORS
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/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, vector: pGEMIJIZF+; Site 1: Eco Ri, Site 2: Not I; Bug of mRNA from Bothrops insularis venom glands were primed with oligo-(dr) and reverse transcribed to CDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agazose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMIJIZ+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
                                                                                                                                                                                                                                                          BM401637 440 bp mRNA linear EST 01-MAY-2002
JL1G1lF Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                     95 IleGluGluGluSerLysLysCysLeuGlyValHisIleGluThrGlyPheHisLysTrp 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria; Squamata, Scleroglossa, Serpentes; Colubroidea; Viperidae, Crotalinae, Bothrops.

1 (bases 1 to 440)

1 (bases 1 to 440)

A buqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL07A (see Reference)
Seq primer: M13F.
                                                                                                                                  222 AGCAATNTTAACTGTGAACGAATTCCTTTNGTCTGGGAG 181
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Matches:
Conservative:
Mismatches:
Indels:

    .440
    /organism="Bothrops insularis"

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Bothrops insularis
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/db_xref="taxon:8723"
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/cione lib="snake Bothrops insularis library IL2"
/cione lib="Snake Bothrops insularis tote=""Organ: venom glands; Vector: pGEM11Zf+; Site 1: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with Oilgo-(dT) and reverse transcribed to CDNA using Superscript Plasmid System for DNA synthesis and Cloning (LifeTechnologies). The cDNAs
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GH025F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                          268
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 654)
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                                                                                                                    1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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A survey of gene expression and diversity in the venom glands of the pitviper anake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                              ---AspAlaGluSerPheCysThrLysGlnValAsn
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This BST corresponds to cluster BITL10A (see Reference)
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 Conservative:
Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:8723"
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                                  Indels:
Gaps:
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54.37$
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 Percent Similarity:
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100 Lys --- LysCysLeuGlyValHisIleGluThrGlyPheHisLysTrpGluAsnPheTyr 118
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were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters at directionally cloned in pGEM11Zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
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Best Local Similarity:
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(without alignments)
264.544 Million cell updates/sec
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| SIDS1/gcgdata/geneseq/geneseqpeembl/AA1990.DAT:
| SIDS1/gcgdata/geneseq/geneseqpeembl/AA1990.DAT:
| SIDS1/gcgdata/geneseqfgeneseqpeembl/AA1992.DAT:
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/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                       170
1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107863 segs, 158726573 residues
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                                                                                                                      sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 sv
                                                                                                                      - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                       US-09-938-114-3
                                                                                                                                                                                   December
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                                                                                                                   OM protein
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                                                                                                                                                                                                                                                                                                       Title:
Perfect
                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Deinagkistrodon ac	Sequence of the pl	Vipera palestinae	Vipera palestinae	Vipera palestinae	Pigmy rattlesnake	N-terminal sequenc	Deinagkistrodon ac	Segmence of polype
SUMMARIES	ID	ı	AAR24427	AAR72232	AAR72234	AAR72236	AAE20178	AAR23889	ABU08799	AAR38225
	DB	24	13	16	16	16	23	13	24	14
	Length	129	116	30	43	127	151	20	146	123
de	Query re Match Length DB	100.0	81.2	79.4	79.4	79.4	78.8	77.6	77.6	77.1
	Score	170	138	135	135	135	134	132	132	131
	Result No.	1	2	3	4	Ŋ	9	7	80	σ

Vipera palestinae Vipera palestinae Vipera palestinae Alylysantinfarctas Snake venom blood Snake venom blood Pigmy rattlesnake Alylysantinfarctas	N-terminal sequenc Sequence of polype Snake venom blood Botrocetin beta su Korean adder snake Snake venom blood	Borrocetin alpha s N-terminal peptide N-terminal peptide Sequence of polype Sequence of polype Sequence of polype N-terminal sequenc		MID-64 KGLA mutant MIJ-64 E62A mutant MIZ-64 YG3A mutant MI3-64 R66A mutant MI4-64 R79A mutant MI5-64 R100A mutan MI6-64 D101A mutan MI6-64 D101A mutan
AAR72231 AAR72235 AAR72235 ABB3143 AAM51540 AAM51544 AAE20179	AAR23886 AAR3822 AAM51541 AAR45157 AAO14521 AAM51543	AAR45156 AAW04861 AAW04862 AAR38227 AAR38231 AAR38226	AAR71978 AAO20975 AAR71979 AAY85627 AAO20973 AAO20981 AAO20982	AA020983 AA020984 AA020985 AA020986 AA020987 AA020989 AA020989
73 73 73 73 73 73 73 73 73 73 73 73 73 7	13 14 17 17 17 17 17 17	114 114 114 114	16 23 21 23 23 23	3333333
32 132 120 30 146 152	28 131 30 125 145	133 30 30 107 122 132 36	38 110 126 126 126 126	126 126 126 126 126 126
7.47 7.47 7.47 7.47 7.47	72.6 70.6 70.0 70.0 70.0	68.8 68.2 68.2 67.1 65.9	655.3 655.3 655.3 655.3	65.3 65.3 65.3 65.3 65.3 65.3
M M M M M M M M	123.5 120 119 119 119	117 116 116 117 112		
110 111 112 115 116	18 20 21 22 23	2 2 2 2 2 2 4 2 2 3 2 4 5 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	33 3 3 3 3 4 3 4 4 4 4 4 4 4 4 4 4 4 4	8 6 6 4 4 4 4 4 8 6 6 7 7 8 4 5

ALIGNMENTS

RESULT 1 ABU08798

Antithrombosis, alpha chain, fibrin hydrolysis, blood clot, enzyme; platelet aggregation, vaso-occulusive disorder; thromboembolic disorder; myocardial infarction; restenosis; cancer; neurodegenerative disease; angiopathic thrombosis; cerebral thrombosis; thromboangitis obliterans; ischemmic cerebral vascular disease; unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema; peripheral arterial occulsion; stroke; atherosclerosis; inflammation; /note= "Antithrombosis enzyme alpha chain N-terminus not encoded by abx93668" Deinagkistrodon acutus antithrombosis enzyme alpha chain. Location/Qualifiers ABU08798 standard; Protein; 129 AA. (first entry) Deinagkistrodon acutus. 02-JUN-2003 chrombosis ABU08798; Region Sey

'note= "Specifically claimed in claim 91 /note= "Encoded by TAT" 1..29 Misc-difference Region

US6489451-B1

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16-NOV-1990;
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                                                                                                                              angina, etc.
                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1994;
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04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukuchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR72232;
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenusly. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.05, micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thrombositonic disorders, including myocardial infarction, restenosis, angipathic thrombosis, cerebral thrombosis, isohaemic cerebral vascular thrombosis unstable angina, acute thrombosis, inschaemic screbral vascular thrombosis unstable stenocardia, chrombosis, pulmonary embolism, deep vein thrombosis, peripheral arterial occulsion, stroke. It is also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents the amino acid sequence of the Deinagkistrodon acutus antithrombosis enzyme alpha chain.
                                                                                                                                              New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of the platelet glycoprotein GPIb inhibitor beta chain
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platelet adherence inhibitor; platelet anti-adhesive; antithrombotic agent; von Willebrand Factor; platelet glycoprotein GPIb-IX complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 170; DB 24;
100.0%; Pred. No. 8.3e-16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                  (HEFE-) HEFEI SIU FUNG USTC PHARM CO LID.
                                                                                                                                                                                                       Claim 12; Column 11; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR24427 standard; Protein; 116 AA.
                      98US-0058740.
                                            97US-043886P
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(first entry)
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29; Conservative
                                                                                                             WPI; 2003-352116/33.
N-PSDB; ABX93668.
                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AA;
                                                                                         Cheng X;
                                                                                                                                                                                   unstable angina
                    10-APR-1998;
                                            10-APR-1997;
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21-NOV-1992
 03-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR24427;
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Best Local
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vipera palestinae, venom; N-terminal fragment, antithrombotic agent, platelet binding; von Willebrand factor.
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                                                                                                                                                                                                                                     Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit thrombus formation; for treatment of arteriosclerosis, atherosclerosis, acute myocardial infarction, chronic unstable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.2%; Score 138; DB 13; Length 116; 75.9%; Pred. No. 2e-11; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vipera palestinae venom derived peptide N-terminal fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72232 standard; peptide; 30 AA
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                                                                                                                                                                                                                                                                                                                                                                                                Example; Fig 6; 5pp; English.
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94JP-0002691.
94JP-0128518.
                                                         (CORT-) COR THERAPEUTICS INC
90US-0614443
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(first entry)
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                                                                                                                                                                                  WPI; 1992-199936/24.
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                                                                                                                     Scarborough RM;
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us-09-938-114-3.rag

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AAR72236;
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                                           RESULT 5
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AAE20178
                                                                                   SO CCC CCC X S X L L L X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
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                AAR72232 is a Vipera palestinae venom derived N-terminal fragment, the full peptide is given in AAR72236. A peptide compsn. comprising AAR72236 and AAR72235 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an antithrombotic agent.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR72234 is a Vipera palestinae venom derived N-terminal fragment, the full peptide is given in AAR72236. A peptide compsn. comprising AAR72236 and AAR72235 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an antithrombotic agent.
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vipera palestinae, venom; N-terminal fragment; antithrombotic agent; platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
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                                                                                                                                                                                                    79.4%; Score 135; DB 16; Length 30; 75.9%; Pred. No. 1.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.4%; Score 135; DB 16; Length 43; 75.9%; Pred. No. 1.6e-11;
                                                                                                                                                                                                                                            6; Indels
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                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                               1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72234 standard; peptide; 43 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 18; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaida K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0002691.
94JP-0128518.
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                                                                                                                                                                                                                     Local Similarity 75.9 tes 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-147392/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vipera palestinae.
                                                                                                                                                            30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 AA;
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04-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR72234;
                                                                                                                                                              Sequence
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Matches
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Matches
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
*555555 *8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; Zsnk2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 79.4%; Score 135; DB 16; Length 127; Similarity 75.9%; Pred. No. 5.6e-11; 22; Conservative 1; Mismatches 6; Indels (
                                                                                                                                                                                                                                            Vipera palestinae, venom; antithrombotic agent; platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pigmy rattlesnake venom gland protein, Zsnk2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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                                                                                                                                                                                         Vipera palestinae venom derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Pages 19-20; 37pp; Japanese.
AAR72236 standard; peptide; 127 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94JP-0002691.
94JP-0128518.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-147392/19.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             Vipera palestinae.
                                                                                                                                                                                                                                                                                                                                                                                WO9509183-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8-SEP-1993;
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ABU08799;
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ABU08799
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                                                                                                                                                                                                                                                                                                                                                The invention relates to new pigmy rattlesnake (Sistrurus miliarius)

venom gland proteins, which affect blood coagulation and platelet

aggregation system. The polypeptides, which affect blood coagulation and

platelet aggregation system, are useful in therapy and diagnostics. The

polypeptides are also useful as an educational tool in laboratory

protein chemistry and antibody production and molecular biology,

protein chemistry and antibody production and analysis. The

polynucleotide or polypeptide can be used as standards or as unknowns

contains by western blotting, protein purification, determining the

weight of expressed polypeptides as a ratio to total protein expressed,

identifying peptide cleavage sites, coupling amino and carboxyl terminal

tags, mass spectromatery, circular dictorism, to determine conformation or

affinity chromatography columns to purify the protein, cloning or

sequencing. The present sequence is Sistrurus miliarius venom gland
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                                                                                                                                                                                                                                                                                which
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                                                                                                                                                                                                                                                                              New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or molecular biology -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal sequence of the earlier eluting subunit PP-beta of the later eluting peak of the platelet antiadhesive peptide (PAA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 23;
Pred. No. 9.5e-11;
2; Mismatches 5;
                              /label= Mature_Zsnk2_protein
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                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 2; 79pp; English
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75.9%;
                                                                                                                                           14-AUG-2000; 2000US-225072P.
14-AUG-2000; 2000US-225087P.
15-AUG-2000; 2000US-225489P.
1C-AUG-2000; 2000US-35699PP.
                                                                                                                        2001WO-US25310
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(first entry)
                                        21..32
49..140
115..132
                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
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                   20..151
                                                                                                                                                                                                                           Bishop
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                                                                                                                                                                                                                                                           N-PSDB; AAD32053
                                        Disulfide-bond
                                                   Disulfide-bond
                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, Zsnk2
                                                                                WO200214364-A2
                                                                                                                        13-AUG-2001;
                                                                                                                                                                                                                           Sheppard PO,
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21-NOV-1992
                                                                                                     21-FEB-2002.
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Best Local 8
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                    Protein
  Peptide
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/note= "Mature antithrombosis enzyme beta chain. Residues 24 to 40 specifically claimed in claim 8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The PAA was purified from a solution of snake venom. The earlier eluting subunit, PP-beta was subjected to Edman degradation for 50 cylces to obtain the sequence in AAR23889. The later eluting sequence - the PP-alpha chain was determined for 31 cycles to give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit thrombus formation; for treatment of arteriosclerosis, atherosclerosis, acute myocardial infarction, chronic unstable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.6%; Score 132; DB 13; Length 50; 75.9%; Pred. No. 5e-11;
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Platelet adherence inhibitor; platelet anti-adhesive; antithrombotic agent; von Willebrand Factor; platelet glycoprotein GPID-IX complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 30; 5pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORT-) COR THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                          91WO-US08516.
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                                                                                                                                      Pseudocerastes persicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scarborough RM;
                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1990;
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94JP-0002691
94JP-0128518
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                                                                                                                        Primeresurus albolabris.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kirby EP, Peng M;
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14-JAN-1994;
10-JUN-1994;
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                                                                                                                                                                                                                                    10-JUN-1993
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           NAME OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour claim after the administration at 0.05 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro/kg. The composition is useful for preventing and treating vaso-occulusive and thrombositic disorders, including myocardial infarction, restenosis, angiopathic thrombosis, cerebral thrombosis, unstable stenocardia, thrombosic, cerebral thrombosis, unstable stenocardia, thrombosities obliterans, pulmonary embolism, deep vein thrombosis, peripheral arterial occulsion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents the amino acid sequence of the prinagkistrodon acutus antithrombosis enzyme beta chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
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                          /label= Unknown
/note= "Encoded by TNN"
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                                                                                                            /label= Unknown
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(first entry)
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Best Local Similarity 72.4:
Matches 21; Conservative
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N-PSDB; ABX93674.
Misc-difference 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AA;
                                                                                  Misc-difference
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                                                                                                                                                                 Misc-difference
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01-0CT-1993
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AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 kDa and about 15 kDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of ARR38224 has been found, characterised by Asp at posn. three in lieu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
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Sequence of polypeptide chain of alboaggregin A (AL-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 131; DB 14;
69.0%; Pred. No. 1.9e-10;
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                                                                   Venom; snake; platelet-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic agent
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                                                                  Length 52;
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                                                                                                 Indels
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Pred. No. 2.9e-10;
3; Mismatches 5;
                                                               76.5%; Score 130; DB 16; 72.4%; Pred. No. 9.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                          Vipera palestinae; venom; antithrombotic agent; platelet binding; von Willebrand factor.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                               3; Mismatches
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                                                                                                                                                  DCPSDWSSHEGHCYKVFRLFKTWEEAEKF 31
                                                                                                                                                                                                                                                                                                                                                           Vipera palestinae venom derived peptide
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                                                                                                                               1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF
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                                                                                                                                                                                                                                              AAR72235 standard; peptide; 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.5%;
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94JP-0002691.
94JP-0128518.
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(first entry)
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                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Vipera palestinae
                                  52 AA;
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14-JAN-1994;
10-JUN-1994;
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Best Local Simil
Matches 21; C
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Local Sim-
21;
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                                  Sequence
                                                                Query Match
                                                                                               Matches
                                                                                                                                                                                                                 RESULT 12
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                                                                                                                                                                                              AAR72231 is a Vipera palestinae venom derived N-terminal fragment, the full peptide is glven in AAR72235. A peptide comparishing AAR72235 and AAR72235 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti-
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vipera palestinae, venom; N-terminal fragment, antithrombotic agent; platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide derived from Vipera palestinae venom - inhibits binding
of platelets to von Willebrand factor, useful as antithrombotic
                                                                                                 Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vipera palestinae venom derived peptide N-terminal fragment.
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                                                                                                                                                                                                                                                                 thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.)
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                                  Kaida K, Kobayashi T;
                                                                                                                                                                                                                                                                                                                                                                                                              1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                 DCPSDWSSHEGHCYKVFRLFKTWEEAEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR72233 standard; peptide; 52 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 18; 37pp; Japanese.
                                                                                                                                                                   Claim 3; Page 17; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaida K,
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.4%;
Matches 21; Conservative
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94JP-0002691.
94JP-0128518.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AJIN ) AJINOMOTO KK.
                                  Fukuchi N, Ishii K,
     (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-147392/19.
                                                                  WPI; 1995-147392/19.
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                                                                                                                                                                                                                                                                                                               32 AA;
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RESULT 11

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The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence is a peptide derived from the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halyxin as blood anticoagulation protein separated from snake venom -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence is the B chain of halyxin.
                                            Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viper; venom; halyxin; anticoagulant; thrombogenesis;
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                                                                                                                                                                                                                                             Length 30;
                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                          Score 127; DB 22;
Pred. No. 1.4e-10;
2; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Son YD;
                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 DCPSGWSSYEGHCYKPFNEQKNWADAENF 52
                                                                                                                                                                                                                                                                                                                               1 DCPSGWSSYEGHCYKPFNEQKNWADAENF
                                                                                                                                                                                                                                                                                                          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF
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                                                                                                                                                                                                                                                                                                                                                                                                                          Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 11-12; 21pp; Korean.
                                                                          Example 1; Page 8; 21pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAMS1544 standard; Protein; 146
                                                                                                                                                                                                                                          74.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2000; 2000KR-0036591
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Matches 20; Conservative
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             WPI; 2001-637330/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for purifying Ahlysantinfarctease thrombase II from the snake wenom of chinese Agkistrodon acutus. The method involves using an anionic exchange column chromatographic process to separate and purify and the repurifying the thrombase in a fast protein purifying work station. It was found that the Ahylysantinfarctase thrombase II consists of two subunits, Subunit A (ABB83142) and Subunit B (the present sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 75.3%; Score 128; DB 23; Length 120; Local Similarity 69.0%; Pred. No. 4.9e-10; les 20; Conservative 2; Mismatches 7; Indels
                                                                         subunit B; snake; venom;
                                                                                                                                                                                                                                                                                                                                                                                  Ahylysantinfarctase thrombase and its production process
                                                                                                                                                                                                                                                                                    (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Son YD;
                                       Ahylysantinfarctase thrombase II subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 5 (Disclosure); 8pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snake venom blood anticoagulant peptide #1.
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                                                                     thrombase II subunit acutus; purification
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        (first entry)
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                                                                     Ahylysantinfarctase
Chinese Agkistrodon
                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-281833/33
                                                                                                                      Agkistrodon acutus
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Matches
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194.853 Million cell updates/sec
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Sequence 5,
Sequence 4,
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Sequence 3
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3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                    US-09-938-114-3
170
1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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US-08-894-403-4
US-07-893-929A-6
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-08-294-859-1
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US-08-481-676-2
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                                                                                                                                                                                                         328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                              Issued_Patents AA;*
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Maximum DB seq length: 200000000
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Match Length DB
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28 111 65.3 130 1 US-07-893-929A-7 Sequence 7, Appli 29 111 65.3 130 5 PCT-US92-10344-7 Sequence 7, Appli 30 111 65.3 149 2 US-08-612-840A-8 Sequence 8, Appli 31 107 62.9 125 5 PCT-US92-10344-3 Sequence 3, Appli 32 107 62.9 125 5 PCT-US92-10344-3 Sequence 3, Appli 34 104 61.2 31 1 US-08-612-840A-8 Sequence 6, Appli 35 104 61.2 31 1 US-08-612-840A-9 Sequence 6, Appli 36 103 60.6 21 2 US-08-612-840A-3 Sequence 6, Appli 36 103 60.6 21 2 US-08-612-840A-3 Sequence 9, Appli 39 102.5 60.3 133 1 US-07-893-929A-9 Sequence 9, Appli 39 102.5 60.3 133 5 PCT-US92-10344-9 Sequence 9, Appli 41 84 49.4 125.7 1 US-08-340-9 Sequence 2, Appli 41 84 49.1 125.7 1 US-08-340-9 Sequence 2, Appli 42 44 1 125.7 1 US-08-340-42 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 45.5 1 US-08-340-4288-49 Sequence 3, Appli 44 79 46.5 912 5 PCT-US95-03747-2 Sequence 2, Appli 45 45.5 1 US-08-340-4288-49 Sequence 3, Appli 45 45.5 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 47 1 US-08-340-4288-49 Sequence 3, Appli 47 1 US-08-340-4288-49 Sequence 3, Appli 44 45 45 1 US-08-340-4288-49 Sequence 3, Appli 44 45 45 1 US-08-340-4288-49 Sequence 3, Appli 44 45 45 1 US-08-340-4288-49 Sequence 3, Appli 44 45 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 US-08-340-4288-49 Sequence 3, Appli 46 1 U
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                                                                      Length 29;
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                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 170; DB 4;
100.0%; Pred. No. 1.1e-15;
live 0; Mismatches 0;
                                                                           100.0%; Score 170; DB 4;
100.0%; Pred. No. 2.3e-16;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFICATION: <union-culture of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the
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STRANDEDNESS: single
JOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-058-740-2
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STREET: 633 West Fifth Street
Suite 4700
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 23:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09058740 Patent No. 6489451 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 129 amino acids
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STATE: California
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Best Local Similarity 100.0
                                                                               Query Match
Best Local Similarity 100.
Matches 29; Conservative
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ZIP: 90071-2066
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US-09-058-740-2
US-09-058-740-3
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RESULT 3

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Pred. No. 2e-11;
2; Mismatches 5; Indels
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COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
                                                                                                                                                                                                                                                                              COMPIETS: USB

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATE: IBM PC compatible
COMPATE: IBM PC compatible
COMPATE: PatentIn Release #1.0, Version #1.25
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614,443A
FILING DATE: 19901116
CLASSIFICATION: 530
ATTORNEY/AGRYT INFORMATION:
NAME: Murashige, Kate H:
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPRAK: (415) 813-5600
TELEFRAK: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mortison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
Sequence 2, Application US/07614443A
Patent No. 5342830
GENERAL INFORMATION:
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCPSDWSSYEGHCYRVFQQEMTWDDAEKF 29
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                                                                                                                           ADVIKESS:
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-294-859-2
; Sequence 2, Application US/08294859
; Patent No. 5679542
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Best Local Similarity 75.9%;
Matches 22; Conservative 2
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NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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RESULT 6
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,676
FILING DATE: 07-JUN-1995
CLASSIFICATION 514
PION APPLICATION DATA:
APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
ATTONNEY/AGENT INFORMATION:
NAME: MANE: NAME: KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDITION & FOOTSTER STREET: 2000 Pennsylvania Ave. N.W., Suite 5500 CIIY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2e-11;
| REGISTRATION NUMBER: 29,959 | REGISTRATION NUMBER: 2803-0003.10 | TELECOMMUNICATION INFORMATION: TELEFAX: (202) 887-1500 | TELEFAX: (202) 887-0763 | TELEFAX: 90-4030 | SEQUENCE CHARACTERISTICS: LENGTH: 117 amino acids | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08481676
Patent No. 5744584
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DCPSDWSSYEGHCYRVFQQEMTWDDAEKF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHAN: (202) 887-150
TELEFAX: (202) 887-0763
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75.9%;
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.99
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    / TOPOLOGY: linear
US-08-294-859-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                       COMPUTER PARAMELE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
OWBUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614,443A
FILING DATE: 19901116
CLASSIFICATION STATE
ATTORNEY/AGENT INFORMATION:
NAME: MALESHORY KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20003.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1879-600
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STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                      NUMBER OF INVENTION: ANTITHROMBOSIS AGENTS NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: Morrison & Foerster STREET: 755 Page Mill Road CITY: Palo Alto STATE: California CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-294-859-5

Sequence 5, Application US/08294859

Patent No. 56799-5

GENERAL INFORMATION:

APPLICANT: SCARBOROUGH, ROBERT M.

ITILE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORTISON & FOERSTER
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FILING DATE: 29-AUG-1994
CLASSIFICATION: 435
                Sequence 5, Application US/07614443A
Patent No. 5342830
GENERAL INFORMATION: APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 50 amino acids
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Best Local Similarity 75.9*
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
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US-07-614-443A-5
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1 DCPSDWSSHEGHCYKVFNLYKTWEDAEKF 29
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                                                                RESULT 9
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Pred. No. 5e-11;
1; Mismatches 6; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,676
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/294,859
FILING DATE: 29-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Morrison & Foerster STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
77.6%; Score 132; DB 1;
Best Local Similarity 75.9%; Pred. No. 5e-11;
Matches 22; Conservative 1; Mismatches
  ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08481676
Patent No. 5744584
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MITASHIGE, KATE H. REGISTRATION NUMBER: 29,959 REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; (202) 887-1500
(202) 887-0763
                                                                                                                                                                                                                                                                                                                                         Query Match 77.6%;
Best Local Similarity 75.9%;
Matches 22; Conservative
                                                                                                                                                                                                          LENGTH: 50 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDENESS: single
1 TOPOLOGY: linear
US-08-294-859-5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington, D.C.
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                    Jaten No. 533660.

Jaten No. 533660.

GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
"TTT.E OF INVENTION: Membrane Glycoprotein Ib
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                                                                                                                                                                                                                          TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Agonists Which Bind To Platele
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEGUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Temple University - Of The Common-ADDRESSER: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 1912.A.
ZIP: 1928. Diskette, 3.50 inch, 720 Kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Alboaggregins: Platelet TITLE OF INVENTION: Agonists Which Bind To Pl TITLE OF INVENTION: Membrane Glycoprotein Ib NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: WAS-DOS
SOFTWARE: WAS-DOS
SOFTWARE: WAS-DOS
SOFTWARE: WAS-DOS
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,929A
FILING DATE: 19920605
CLASSIPICATION 435
RAPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATORNEY/AGENT INFORMATION:
NAME: MANDER MAINTEN ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MANDER ASOFT MA
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Sequence 4, Application US/07893929A Patent No. 5336667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kirby, Edward P. APPLICANT: Peng, Man-ling
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AMINO ACID
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Best Local Similarity 69.0
Matches 20; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Philadelphia

1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29

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Pred. No. 5.7e-09;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                              Score 120; DB 1; Length 131;
Pred. No. 5.7e-09;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9210344
; Sequence 1, Application PC/TUS9210344
; GENERAL INFORMATION: General P. APPLICANT: Firby, Edward P. APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Abongsregins: Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
TITLE OF INVENTION: Membrane Glycoprotein Ib
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 10
ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: DISPACLUE, 3.50 AMEDIA, 720 AMEDIA COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
FILING DATE: 19921201
FILING DATE: 19921201
FILING DATE: December 3, 1991
ATTORNEY AGENT INFORMATION:
NAME: MODIACO, DATIEL A.
NAME: MODIACO, DATIEL A.
REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPHONE: (215) 568-549
TELERAX: (215) 568-549
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
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(215) 568-5549
                                                                                                                                                                                                                                                               Query Match 70.6%;
Best Local Similarity 65.5%;
Matches 19; Conservative 5
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Matches 19; Conservative
                                                                                                                                                             LENGTH: 131 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                      TOPOLOGY: linear
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TELEFAX: (
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GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.

APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDESS: 10
CORRESPONDESSE: Temple University - Of The Common-ADDRESSE: wealth System of Higher Education
STREET: Wealth System of Higher Education
STREET: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: DISACTC, 3.50 inch, 720 Kb
COMPUTER: IBM PS/C
COMPUTER: WORLD SYSTEM: MS-DOS
SOFTWARE: WORDPEFFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  6056-126 (CIP) 1
                                                                                                                        Diskette, 3.50 inch, 720 Kb
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FILING DATE: 19920605
CLASSIFICATION: 435
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720
COMPUTER: IBM FS/2
COMPUTER: IBM FS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CTELEPRENCE/DOCKET NUMBER: 61566-126 (CTELEPRENCE/DOCKET NUMBER: 61568-8393
TELEPRAK: (215) 568-8393
TELEPRAK: (215) 568-5549
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APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/07893929A
Patent No. 5336667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: None INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: 123 amino acids
AMINO ACID
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Best Local Similarity 69.03
Matches 20; Conservative
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STATE: Pennsylvania
                                                Pennsylvania
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                                                                                       19122
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TOPOLOGY:
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Pred. No. 4e-09;
1; Mismatches 9; Indels
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Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent No. 5972681
Patent Norden Calcium-Requiring Prothromein Activator
Patent Patent Als-653P
CURRENT APPLICATION NUMBER: US/08/894,403A
CURRENT FILING DATE: 1997-08-18
NUMBER OF SEQ. ID NOS: 7
COFFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.1%; Pred. No. 4e-09;
Matches 18; Conservative 2; Mismatches 9; Indels
                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MORITA, Takashi
TITLE OF INVENTION: A.5-6.54
FILE REPERENCE: 45.5-6.54
CURRENT APPLICATION NUMBER: US/08/894,403A
CURRENT FILING DATE: 1997-08-18
SOFTWARE: PALENTIN Ver: 2.0
SOFTWARE: PALENTIN Ver: 2.0
TYPE: PRT
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APPLICANT: Kirby, Edward P.
APPLICANT: Pens, Man-ling
TITLE OF INVENTION: Alboagregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Agonists Minch Bind To Platelet
TITLE OF INVENTION: Agonists Wendrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
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; Patent No. 5972681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ_ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-894-403-4
                                                                                                                                                                                                                                                                                                                                                                 CORGANISM: Arabidopsis thaliana US-08-894-403-3
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.5%;
Matches 19; Conservative
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US-07-893-929A-6
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US-08-894-403-4
JS-08-894-403-3
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                                                                                                                                                                                                                                       FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 435
FILING DATE: DOCEMBER: 07/803,630
FILING DATE: DOCEMBER: 3, 1991
FILING DATE: DOCEMBER: 3, 1991
NAME: MONGO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
                                                        COUNTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
COMPUTER: MOSTEM: MS-DOS
COMPUTER: MOSTEM: MS-DOS
CONTWARE: MOSTEM: MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,929A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELERX: No. 533667e
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 107 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 65.5
Matches 19; Conservative
                        Pennsylvania
U.S.A.
Philadelphia
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                     STATE: P. COUNTRY:
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Sequence 31252, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Appli
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                                                                                                     December 8, 2003, 09:54:55; Search time 11.9314 Seconds (without alignments) 452.044 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, A Sequence 8, A Sequence 10, Sequence 11,
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Sequence 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
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| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-114-3
US-09-929-130-2
US-09-929-230-2
US-10-226-420-2
US-09-929-230-5
US-09-929-730-3
US-09-929-730-3
US-09-929-230-8
US-09-959-763-10
US-09-929-230-11
US-10-226-420-11
US-10-226-420-11
US-10-929-230-11
US-10-029-938-31252
US-10-029-386-31252
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                        684280 segs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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seg length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
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US-09-965-528-2	US-U9-801-438-2	-055-137-	001	1-C44-98T-	-195-970-	-195-970-6	0-189-123-7	φ		0-226-420-1	-020-104-	10-050-704-27	US-10-050-704-272	-237-49	-242-074	1	- 1	-243 - 261	-243-282	-243-402	0 - 243 - 431	10-245-164	0 - 244 - 972	-197-942	-238-19	-245-0	-245 - 103	-245-107	-245-1
-60-SI	200-20	00-01				US-10-	US-10-18	-60-SN	US-09-929	US-10-	US-10-	US-10-	US-10-	US-10.	US-10	US-10	US-10-242	US-10-	US-10-243	US-10-243	US-10	US-10	US-10	US-10	US-10	US-10	US-10	US-10	US-10
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83	82	282	78	82	82	82	82	81	77	77	16	16	16	76	76	16	16	16	76	16	16	92	16	76	16	16	16	16	16
16	17	81	13	20	21	22	23	2.5	25	56	27	28	50	0 6	3.6	3.6	3.0	3.0	, r.	3.6	3.7	. 00	0 6	7 4	7 4	24	4.4	4	4.5

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Length 129;
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Pred. No. 1.6e-10;
2; Mismatches 5; Indels
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                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                          APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
UNDMER OF SEQ ID NOS: 14
SOFTWARE: PREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10226420
Publication 0. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: BISHOP, Paul D.
APPLICANT: BISHOP, Paul D.
                                                       100.0%; Score 170; DB 11;
100.0%; Pred. No. 1.9e-15;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 134; DB 12;
Pred. No. 1.6e-10;
2; Mismatches 5;
                                                                                                                                     1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                    1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
                                                                                                                                                                                                                                                                         Sequence 2, Application US/09929230
Patent No. US20020161203A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09929230
Patent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.8%;
Best Local Similarity 75.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Sistrurus miliarius
                                                 Query Match
Best Local Similarity 100.0
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                US-09-938-114-2
                                                                                                                                                                                                                                                  US-09-929-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-929-230-2
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US-10-226-420-2
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Matches
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                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                   Length 29;
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US-09-938-114-2
; Sequence 2, Application US/09938114
; Fublication No. US20030022350A1
; GENERL INFORMATION:
    APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and Hui-Ran Chen
                                                                                                                                                                                                                                                                       Ouery Match

100.0%; Score 170; DB 11;
Best Local Similarity 100.0%; Pred. No. 4.1e-16;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STORBUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,114
                                                                                                                                                                                                                                                                                                                                                   1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                        1 DCSSDWSSYEGHCYKVFKOSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Chen, Anthony C.
REGISTRATION NUMBER: 38,673
REPERENCAPIONER: 233/298
TELECOMMUNICATION:
TELEPHONE: (213) 955-0440
                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,740
FILING DATE: <Unknown>
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ 1D NO: 2:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
                  TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
                                                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 129 amino acids
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                                                           Score 111; DB 10; Length 149;
Pred. No. 2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.7%; Score 110; DB 12; Length 144; 58.6%; Pred. No. 2.6e-07; Live 5; Mismatches 7; Indels
                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09929230
Fatent No. US20020161203A1
GENERAL INFORMATION:
TAPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION UNMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 64.7%; Score 110; DB 10; Similarity 58.6%; Pred. No. 2.6e-07; 17; Conservative 5; Mismatches 7;
                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                           1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                   26 ECPSGWSSYDRYCYKPFKQEMTWADAERF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 DCPSDWYAYDQYCYRVIKQLRTWDDAERF 40
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US-09-969-763-10
; Sequence 10, Application US/09969763
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Publication No. US20030157686A1
GENERAL INFORMATION:
                                                                                                                           65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT (CRANISM: Sistrurus miliarius US-10-226-420-8
                                         ; TYPE: PRT
; ORGANISM: Crotalus harridus
US-09-969-763-3
                                                                                                                                                                    18; Conservative
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Best Local Similarity 58.64
Matches 17; Conservative
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Matches 18; Conserv
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Matches 17; Conserv
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US-09-929-230-8
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                     LENGTH:
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Publication No. US20020198363A1
GENERAL INFORMATION:
APPLICANT: FURUCHI, NAOYUKI
APPLICANT: KITO, MORIKAZU
APPLICANT: KITO, MORIKAZU
APPLICANT: FUTAKK, FUME
APPLICANT: SUJUKI, FINCHIRO
APPLICANT: SHIKAWA, KOHKI
APPLICANT: SHIKAWA, KOHKI
APPLICANT: SHIKAWA, NOHLISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: YAMADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING 1
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74.7%; Score 127; DB 10; Length 152;
Best Local Similarity 72.4%; Pred. No. 1.4e-09;
Matches 21; Conservative 2; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%; Score 127; DB 12; Length 152; 72.4%; Pred. No. 1.4e-09; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-10-226-420-5

Sequence 5, Application US/10226420

Publication No. US20030157686A1

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul D.

TITLE OF INVENTION: Paul D.

TITLE OF INVENTION: RATTLESNARE VENOM GLAND PROTEINS

FILE REPERENCE: 00-72

CURRENT APPLICATION NUMBER: US/10/226,420

CURRENT FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE FALSEQ for Windows Version 4.0
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION VMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASELSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: JP 2000-305279
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                        TYPE: PRT
CRGANISM: Sistrurus miliarius
US-09-929-230-5
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Best Local Similarity
Matches 21, Conserve
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LENGTH: 152
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LENGTH: 152
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US-09-969-763-3
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APPLICANT: GONDOH, KEIKO
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: YAMADA, NADYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TI-
FILE REFERENCE: 214760US0
CURRENT APPLICATION NUMBER: US/09/969,763
CURRENT APPLICATION NUMBER: US 2000-10-25
PRIOR APPLICATION NUMBER: UP 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Publication No. US20030194704A1
Septement Sequence 31252, Application No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: PENNY GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GH
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AECMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DAFE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31252
LENGTH: 52
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Pred. No. 1.8e-05;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Length 158;
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Pred. No. 1.6e-05;
6; Mismatches 8
CURRENT APPLICATION NUMBER: US/10/226,420; CURRENT FILING DATE: 2002-08-21; NUMBER OF SEQ ID NOS: 14; SCOTYRARE: FastSEQ for Windows Version 4.0; SEQ ID NO 11; LENGTH: 158; TYPE: PRT
TYPE: PRT
TYPE: PRT
CRGANISM: Sistrurus miliarius
US-10-226-420-11
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Publication No. US20020198363A1
GENERAL INFORMATION:
APPLICANT: FUKUCHI, NAOYUKI
APPLICANT: KITO, MORIKAZU
APPLICANT: KAYAHARA, TAKASHI
APPLICANT: FUTAKI, FUMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.2%;
Matches 16; Conservative
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Best Local Similarity 51.7%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISHIKAWA, KOHKI
APPLICANT: SUZUKI, BIICHIRO
APPLICANT: GONDOH, KBIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-029-386-31252
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APPLICANT: SUZUKI, EIICHIRO
APPLICANT: SUZUKI, EIICHIRO
APPLICANT: GONDOH, KEIKO
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NOBUHISA
APPLICANT: SHIMBA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING
FILE REPERENCE: 214760USO
CURRENT APPLICATION NUMBER: US/09/969,763
CURRENT FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
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58.8%; Score 100; DB 10; Length 110;
Best Local Similarity 58.6%; Pred. No. 4.5e-06;
Matches 17; Conservative 3; Mismatches 9; Indels
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; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FRASESQ for Windows Version 4.0
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19.10-226-420-11
19.10-226-420-11
19.10-206-420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: SYNTHETIC PEPTIDE US-09-969-763-10
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; ORGANISM: Sistrurus miliarius
US-09-929-230-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: ARTIFICIAL SEQUENCE
                                  No. US20020198363A1
                                                                                                                                       KITO, MORIKAZU
KAYAHARA, TAKASHI
FUTAKI, FUMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-929-230-11
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LENGTH: 158
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LENGTH: 110
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| Publication No. US20030148408A1 |
| GENERAL INFORMATION: |
| APPLICANT: Frantz, Gretchen |
| APPLICANT: Fillan, Kenneth J. |
| APPLICANT: Polakis, Paul |
| APPLICANT: Polakis, Paul |
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| APPLICANT: Polakis, Paul |
| APPLICANT: Polakis, Paul |
| APPLICANT: Wu, Thomas |
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49.4%; Score 84; DB 12; Length 1321;
Best Local Similarity 42.3%; Pred. No. 0.0082;
Matches 11; Conservative 4; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
49.4%; Score 84; DB 12; Length 52;
Best Local Similarity 42.3%; Pred. No. 0.0003;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                         CTHER INPORMATION: MAP TO AC005254.1

COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.58

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74

CHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74

US-10-029-386-31252
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-10-241-220-82
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPENO spool/1080998114/runat 08122003 091000 22849/app_query.fasta_1.725
-Q=/cgn2 1/USPENO spool/10809938114/runat 08122003 091000 22849/app_query.fasta_1.725
-DB=GenEmbl -QFMT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HRAPSIZE=550 -MINLEN=0 -NAXLEN=20000000
-USRE-US09938114 @CGN 1 1 3707 @runat 08122003 091000 22849 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                      December 8, 2003, 12:41:24; Search time 1230.93 Seconds (without alignments) 963.811 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                              OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                170
1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2888711 segs, 20454813386 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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7.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: gb_ba: *

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4: gb_om: *

5: gb_ov: *

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9b_pl: *

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                Run on:
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29: em_vi:*
30: em_htg:hum:*
31: em_htg:inv:*
32: em_htg:inv:*
33: em_htg:mus:*
34: em_htg:nus:*
35: em_htg:nus:*
36: em_htg:nus:*
37: em_htg:vr:*
38: em_sy:*
39: em_htg:vr:*
41: em_htg:nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption		76420 Deinagki	1758 Delnagki	5880 Deinagki	647 Deinagki	5421	7201	516 Agkistro	1761 Deinagki	88	32 Trimeresur	6 Deinagk		6 Deinagki	AF350324 Delnagkis	S	_	Callosel	AY091760 Deinagkis		Trimeres	AF387100 Deinagkis	AX427203 Sequence	Arizosto Gloyands	AFISURZ/ GIOYGIUS	oo Deinagki	Crotalus d	206 Sequenc		521 Deinagk	58948 Echis ca	0648	Sequenc	AX404807 Sequence		27207 Sequence	44900 Callose	209 Sequence	091759 Deinagki	645 D	99322	49340	99321	309 G	19615
SUMMARIES	ID	1 1	91	9175	3688	964	42	720	961	AY091761	588	FIXB	9386	AR259041	2	AF350324			AF244901	AY091760	TFLFIXA	AB046491	AF387100	AX427203	AF125310	AF190827	AE102E02	CDRNACVXB	AX427206	AR259035	AF463521			AR026653			2720	4490	2720	09175	40	9932	4934	X0993	30	B01961
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	Result No.	1	1	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	57	24	270	27	28	23	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

LOCUS DEFINITION

AF176420

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

AUTHORS TITLE

JOURNAL REFERENCE AUTHORS

REFERENCE

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AY091758 497 bp mRNA linear VRT 13-MAY-2002
Deinagkistrodon acutus clone 2100590 ACF 1/2 A-chain mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MGRFIFVSFGLLVVFLSLSGTAADCSSSWSSYEGHCYKAFKQSK
TWADAESFCTKCVNGGHLPSTESSGRADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQC
SISTEWSDGSSISYENVIELESEKKCLGVHKATGFRKWENFYCEQRDPFVCEA"
102 c 1143 g 117 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 GATTGTTCCTCTAGTTGGTCCTCCTATGAGGGCATTGCTACAAGGCCTTCAAACAATCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu,H., Xiang,K., Wang,Y. and Liu,J.
Direct Submission
Submitted (22-MR-2002) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, School
Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu,H., Xiang,K., Wang,Y. and Liu,J.
A chain of ACF 1/2 from Deinagkistrodon acutus Unpublished
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/note="C-type lectin family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Deinagkistrodon acutus"
/mol_type="mRNA"
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Conservative:
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Indels:
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/product="ACF 1/2 A-chain"
                                                                                                         218 AAGACCTGGACAGATGCAGAGAGCTTC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAM22786.1"
/db_xref="GI:20562937"
                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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                                                                21 LysThrTrpThrAspAlaGluSerPhe
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                                                                                                                                                                                                                                                          AY091758
AY091758.1 GI:20562936
                                                                                                                                                                                                                                                                                                                         Deinagkistrodon acutus
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                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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Yu,H.-X., Xiang, K.-J., Wang, Y. and Liu, J.

Yu,H.-X., Xiang, K.-J., Wang, Y. and Liu, J.

A chain of agkiaacutacin from Deinagkistrodon acutus
Unpublished

4 (Dases 1 to 733)

S Cheng, X., Liu, J., Li, B.X.Y. and Qian, Y.

Direct Submission

Life-Science, Huangshan Road, Hefei, Anhui 230027, China, School of Life-Science, Huangshan Road, Hefei, Anhui 230027, China, S.

Yu,H.-X., Xiang, K.-J., Wang, Y. and Liu, J.

Direct Submission

Submitted (123-APR-2002) Dept. of Biochemistry and Molecular Biology, University of Science and Technology of China, School of Life-Science, Huangshan Road, Hefei, Anhui 230027, China, School of Science update by submitted Road, Hefei, Anhui 230027, China Sequence update by submitter version replaced gi:6715112.

Location/Qualifiers

You
             AF176420 733 bp mRNA linear VRT 30-APR-2002 Delnagkistrodon acutus clone 2100490 agkisacutacin A chain mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MGRFIFVSFGLLVVFLSLSGTAADCSSGWSSYBGHCYKVFKQSK
TWTDARSFCTKQVNGGHLYSIBSSGRADFVGQLIAQKTKSAKTHVWIGHRAQNKEKQC
SIEWBQDGSSISYBNWIEBEKKCLGVHIETGFHKWENFYCEQQDPFVCEA"
173 c. 173 c. 204 g. 165 t.
                                                                                                                                                                                                                                                                                                                                                                                   Huang, W. and
                                                                                                                                                                              Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Liepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, 1 (bases 1 to 733)

Yu,H.-X., Xiang,K.-J. and Liu,J.
Yu,H.-X., Xiang,K.-J. and Liu,J.
Subha. Sequencing and analysis of eleven C-type lectin-like protein subunits from Agkistrodon acutus
Sheng wu hua hsueh yu sheng wu wu li hsueh pao (2002) In press Chases 1 to 733)
Chases 1 to 733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="consists of two heterologous subunits (A and B chains) linked by an inter-subunit disulfide bond; c-type lectin family member"
                                                                                                                                                                                                                                                                                                                                                                                                 Liu, J.
Agkisacutacin, a new fibrinolytic & anti-platelet protein from Unpublished
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0 10
0 0 0 0
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/mol_type="mRNA"
/db_xref="taxon:36307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="agkisacutacin A chain"
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/db_xref="G1:20273044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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Conservative:
Mismatches:
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89. .547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="2100490"
                                                                                              AF176420.2 GI:20273043
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163.00
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                                                     complete cds. AF176420 AY091757
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Best Local Similarity:
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1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20

x AF176420 (1-733)

US-09-938-114-3 (1-29)

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Query Match:

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BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF176421 458 bp mRNA linear VRT 19-JAN-2000
Deinagkistrodon acutus agkisacutacin B chain mRNA, complete cds.
AF176421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWADAEKFCTQQHKGSHLASFHSSEBADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKW
SDGTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTYSFVCKFQA"
                                                                                                                                                                                Wang, W.-J., Ling, Q.-D. and Huang, T.-F.
Molecular structure and functional characterization of agglucetin,
a tetrameric glycoprotein Ib-binding protein, from Formosan pit
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eupidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Corcalinae, Deinagkistrodon.
1 (bases 1 to 458)
Cheng, X., Qian, Y., Liu, Q., Li, B.X.Y., Ding, J., Xu, Z., Huang, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GATTGTCCCTCTGAGTGGTCCTCCTATGAAGGGCATTGCTACAAGGCCTTCAAACAATCT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61. .501
/note="platelet agglutination inducer; glycoprotein Ib
agonist"
                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-2002) Department of Nursing, Chang Gung Instiof Technology, 261, Wen-Hwa 1 Rd., Kwei-Shan, Tao-Yuan, Taiwan 333-03, R.O.C.
                                                               A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist Thromb. Haemost. 86 (4), 1077-1086 (2001)
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224
11
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173 c 172 g 162 t
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/organism="Deinagkistrodon acutus"
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Matches:
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Mismatches:
Indels:
      Viperidae; Crotalinae; Deinagkistrodon.
1 (bases 1 to 688)
Wang,W.J. and Huang,T.F.
                                                                                                                                                                                                                                                              Unpublished
3 (bases 1 to 688)
Wang,W.-J., Ling,Q.-D. and Huang,T.-F.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:36307"
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130. .498
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86.21%
82.76%
87.06%
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Best Local Similarity:
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TWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQC
SIEWSDGSSISYENWIEEESKKCLGVHKATGFRKWENFYCEQRDFFVCEA"
                                                                                                                                                                                                                                                                                                             Submitted (66-JAN-2000) Tomohisa Ogawa, Tohoku University, Graduate School of Agricultural Science; 1-1, Tsutusmidori Amamiyamachi, Abba-ku, Sendai 981-8555, Japan (B-mail:ogawa@biochem.tohoku.ac.jp, URL:http://www.agri.tohoku.ac.jp/hoozo/, Tel:81-22-717-8807)
Fax:81-22-717-8807)
Location/Qualifiers
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                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Deinagkistrodon.
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Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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Deinagkistrodon acutus agglucetin-beta 1 subunit precursor, mRNA, complete cds.
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                                                                                                                                     Tani, A., Ogawa, T., Nose, T., Nikandrov, N.N., Deshimaru, M., Chijiwa, T., Chang, C.C., Fukumaki, Y. and Ohno, M. Characterization, primary structure and molecular evolution anticoagulant protein from Agkistrodon actus venom Toxicon 40 (6), 803-813 (2002)
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    . .656
    /organism="Deinagkistrodon acutus"

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/gene="acp-a"
a 148 c 1
                      Deinagkistrodon acutus
Deinagkistrodon acutus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="acp-a"
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155.00
89.66%
89.66%
91.18%
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Ogawa, T. and Tani, A.
Direct Submission
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RESULT

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/translation="ITVSTGELLVVFLSLSGTGADCPSDWSSYDQHCYKVFSELKTWDD Arranslation="ITVSTGELLVVFLSLSGTGADCPSDWSSYDQHCYKVFSELKTWDD ARRANGTGATGASTASIHSSEEBAFVGKLASQTLKFTSMWIGLKDLWKECKWQWSDDT KLDYKAWTRRPYCTWVVYTDRIFWRNRGCEKTVSFVCKFQARSGDPAV"
112 c 123 g 119 t
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Agkistrodon blomhoffi mRNA for mamushigin beta, complete cds.
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Sakurai,Y. and Fujimura,Y.
Direct Submission
Submitted (10-NOV-1998) Yoshihiko Sakurai, Nara Medical University,
Department of Blood Transfusion Medicine; Shijo-cho 840, Kashihara,
Nara 634-8522, Japan (B-mail:ysakurai@nmu-gw.cc.naramed-u.ac.jp,
Tel:81-744-22-3011(ex.3288), Fax:81-744-29-0771)
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TWEDAEKFCTQQRKESHLVSFHSSEEVDFVVSMTWPLLKXDFVWIGLNNIWNECMVEW
TDGTRLSHWANITESECLAAKTTDNQWLSRPCSRTYNVVCKFQE"
153 c 173 g 164 t
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1 (sites)
Sakurai,Y., Fujimura,Y., Kokubo,T., Imamura,K., Kawasaki,T., Handa,M., Suzuki,M., Matsui,T., Titani,K. and Yoshioka,A.
The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from pakistrodon halys blomhoffii venom
Thromb. Haemost. 79 (6), 1199-1207 (1998)
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'protein id="BAA34425.1"
'db_xref="GI:3882119"
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/codon_start=1
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Agkistrodon blomhoffi
Agkistrodon blomhoffi
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/db_xref="rexon:36307"
/tissue_type="venom"
3. 443
/note="agkisacutacin consists of two heterologous subunits
(A and B chains) linked by an inter-subunit disulfide
bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGRFIFVSFGLLVVFLSLSGTAADCPSDWSSYEGHCYKPFDEPK
TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKW
SDGTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCKFQA"

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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Sistrurus.
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                                                                                                                                              of
                                                                     2 (bases 1 to 458)
Cheng.X., Liu,J., Li,B.X.Y. and Qian,Y.
Direct Submission
Submitted (08-AUG-1999) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, School
Life-Science, Huangshan Road, Hefei, Anhui 230027, China
Location/Qualifiers
                Agkisacutacin, a new fibrinolytic & anti-platelet protein from Agkistrodon acutus venom Unpublished
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fproduct="agk!sacutacin B chain"
protein id="AAP56287.1"
db_xref="GI:6715115"
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/mol_type="genomic DNA"
/db_xref="taxon:8758"
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Rattlesnake venom gland proteins
Patent: WO 0214364-A 1 21-FEB-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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/codon_start=1
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C bases 1 to 592)
Ogawa, T. and Tani, A.
Direct Submission
Submitted (14-JAN-2000) Tomohisa Ogawa, Tohoku University, Graduate School of Agricultural Science; 1-1, Tsutusmidori Amamiyamachi, Aoba-ku, Sendai 981-8555, Japan (E-mail:ogawa@biochem.tchoku.ac.jp, URL:http://www.agri.tchoku.ac.jp/hoozo/, Tel:81-22-717-8808,
                                                                              AB036881 592 bp mRNA linear VRT 23-MAY-2002 Deinagkistrodon acutus acp-b mRNA for anticoagulant protein-B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="anticoagulant protein-B"
/protein_id="BAB20441.1"
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SNAAMLKYTDWAEESYCVYFKSTNNKWRSITCRMIANFVCEFQA"
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Deinagkistrodon acutus
Belnagkistrodon acutus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamaca, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Deinagkistrodon.
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                                                                                                                                                                                                                                                                                          Tani, A., Ogawa, T., Nose, T., Nikandrov, N.N., Deshimaru, M., Chijiwa, T., Chang, C.C., Fukumaki, Y. and Ohno, M.
Characterization, primary structure and molecular evolution of anticoagulant protein from Agkistrodon actus venom
Toxicon 40 (6), 803-813 (2002)
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/db_xref="taxon:36307"
/tissue_type="venom gland"
1. .592
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         130 AAAAACTGGGCGGATGCAGAGAATTTC 156
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SNAAMLKYTDWAEESYCVYFKSTNNKWRSITCRMIANFVCEFQA"
107 c 125 g 119 t
                                                                                                                                                               Deinagkistrodom acutus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
1 (bases 1 to 478)
Yu,H., Xiang,K., Wang,Y. and Liu,J.
B chain of ACF 1/2 from Deinagkistrodon acutus
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Direct Submission
Submission
Submission
Biology, University of Science and Technology of China, School of Life Science, Huangsham Road, Hefei, Anhui 230027, P.R. China
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Deinagkistrodon acutus clone 2101 ACF 1/2 B-chain mRNA, complete
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/note="C-type lectin family member"
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AY091761.1 GI:20562942
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TEEADFVYKLAFQTFDYGIFWMGLSNIWNQCNWQWSNAAMIKKTDWAEBSYCVYFKST
NNKWRSITCRNIAFVCFEQA 91 t
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        Zha, X.D., Ren, B., Liu, J. and Xu, K.S. Genomic DNA sequence of b chain of Agkisasin, a C-type lectin-like protein from Agkistrodon acutus venom, and its evolutionary significance
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Li,B.X. and Cheng,X.
Antithrombosis enzyme from the snake venom of agkistrodon acutus
Patent: US 6489451-A 12 03-DEC-2002;
                                                                         Unjublished

2 (bases 1 to 369)

2 hases 1 to 369)

2 hases 2 Liu, J. and Xu, K.S.

Direct Submission

Submitted (07-MAY-2003) Biology, School of Life Science, Anhui
University, 3 Feixi Road, Hefei 230039, China

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:36307"

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/product="agkisasin-b"
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107 c 114 g
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NWADAENFCTQQHAGGHLVSFQSSEEADFVVKLAFQTFGHSIFWMGLSNVWNQCNWQW
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                                                                                                                                                                                                                                                                                                                                   Submitted (02-FEB-1996) Takashi Morita, Meiji College of Pharmacy, Biochemistry; 1-22-1 Yatocho, Tanashi, Tokyo 188, Japan (Tel:0424-21-0101(ex.429), Fax:0424-21-1489) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinagkistrodon acutus
Deinagkistrodon acutus
Evkaryota: Metazota; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                                         factor IX/factor X binding protein B chain.
Trimeresurus flavoviridis
Trimeresurus flavoviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Uppridae; Crotafinae; Trimeresurus.
(Dases 1 to 698)
Matsuzaki,R., Yoshiara,E., Yamada,M., Shima,K., Atoda,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                           Morita,T. cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="factor IX/factor X binding protein B chain"
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 Trimeresurus flavoviridis mRNA for factor IX/factor X binding
                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 220 (2), 382-387 (1996)
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Deinagkistrodon acutus agkisasin-b gene, partial cds.
AY293866
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                    protein B chain, complete cds
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VRT 25-MAR-2001
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1. 375
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INNKWRSITCRMIANFVCEFQA"
                                                                                                                                            Deinagkistrodon actius
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Libases (Totalinae; Deinagkistrodon.
Libases 1 to 574)

Zha,X. and Xu,K.
Direct Submission

Submitted (20-FEB-2001) Biochemical and Genetic Engeneering Drugs,
National Institute for Control of Phamaceuticals and Biological
Products, Tiantan Ximen, Xili Street 2, Beijing 10050, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF197915
G14 bp mRNA linear VRT 01-NOV-2000 Gloydius halys halyxin B-chain precursor, mRNA, complete cds.
AF197915
AF197915.1 GI:11066255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GATTGICCTTCTGATTGGTCCTCTTATGAAGGCCATTGCTACAAGCCCTTCAATGAACTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gloydius halys (halys viper)
Gloydius halys
Gloydius halys
Gloydius halys
Ebidacycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
1 (bases 1 to 634)
Koo,B.H., Sohn,Y.D., Kim,D.S., Jang,Y.S. and Chung,K.H.
A Novel Coagulation Factor Xa Inhibitor from Korean Snake
(Agkistrodon halys) venom
                              AF350324 1inear VR
Deinagkistrodon acutus agkisasin-b mRNA, complete cds.
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21
2
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    .574
    /organism="Deinagkistrodon acutus"

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Mismatches:
Indels:
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2 (bases 1 to 634)
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AUTHORS
TITLE
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AF197915
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                                                                                                                                                                                                                                                                                  ALUY1756 478 bp mRNA linear VRT 13-MAY-2002 Deinagkistrodon acutus clone 2100488 agkisacutacin B-chain mRNA, complete cds.
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SDGTKLDYXDWREQFECLYSFVVNNEWLSMDCGTTCSFVCKFQA"
109 c 126 g 117 t
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72 GATTGTCCCTCTGAGTGGTCCTCCTATGAAGGCATTGCTACAAGCCCTTCGATGAACCT 131
                                                                                             AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                             Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-MAR-2002) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, School of
Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viperidate: Crotalinae; Cortalinae; Coll. (Dases 1 to 478)
Yu, H., Xiang, K., Wang, Y. and Liu, J.
B chain of agkisacutacin from Deinagkistrodon acutus Unpublished
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Matches:
Conservative:
Mismatches:
Indels:
  Indels:
Gaps:
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Yu,H., Xiang,K., Wang,Y. and Liu,J.
Direct Submission
                                                                                                                                                                                                         132 AAGACCTGGGCAGATGCAGAGAAATTC 158
                                                                                                                                                                         LysThrTrpThrAspAlaGluSerPhe 29
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77.65$
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Sohn, Y.D., Koo, B.H., Kim, D.S., Jang, Y.S. and Chung, K.H.

REFERENCE AUTHORS

US-09-938-114-3 (1-29)

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RESULT 14

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Similarity:

Percent Similarity: Best Local Similari

Query Match:

Alignment Scores:

Pred. No.:

Score:

BASE COUNT

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                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (22-OCT-1999) Cardiovascular center, Yonsei University
College of Med., 134 Shinchon-dong, Seoul 120-752, Republic of
                                634
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Conservative:
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Indels:
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/product="halyxin B-chain"
142 c 157 g 155 t
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Search completed: December 8, 2003, 16:08:45 Job time : 1231.93 secs

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-DB=N_Geneseq_195uno3 -QFPT=fastap-SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODES=LOCAL -OOTFMT=-pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                       OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2552756 seqs, 1349719017 residues
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Ygapop 10.0 , Ygapext
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Maximum DB seq length: 200000000
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Scoring table:

Searched:

Perfect score:

Run on:

Sequence:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, | SIDS1/gogdata/geneseq/geneseqn-embl/NA1995.DAT:*
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Database :

is derived by analysis of the total score distribution. and

SUMMARIES

			æ			SUMMAKIES	
Re '	Result No.	Score	Query	Length	DB	ID	escription
	Н (134	78.8	483	24	AAD32053 P	Pigmy rattlesnake
	(1)	132	77.6	454	25		encodin
	n 4	127	7.4.	723	77		Snake venom blood
	'n	119	70.0	453	4 4		Pigmy rattlesnake
	9	119	70.0	583	24		ק ק
	7	119	70.0	601	22		enom b
	သော	115	67.6	456	24		/ rattles
	10	111	65.3	440	7 7		encodin
	11	111	65.3	069	217		Snake venom antith
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	13	110	64.7	580	24		attlesnake
	4.	103	9.09	432	24		Pigmy rattlesnake
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	9 5	76	57.1	725	24		Pigmy rattlesnake
	, œ	¥ 5	52.3	774	<u>.</u>		Snake venom protei
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	22	82	48.2	495	24		DNA encoding nowel
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	4. C	74		857	22		cDNA encodi
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답 \$	18-JI	-JUN-2002	(first	st entry)	<u>د</u>		
OE Y	Pigmy	rattl	esnake	venom	gland	l protein, Zsnk2 gene.	
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K K K	plate	rat let	rattlesnake; et aggregatic	veno	m glan ene; Z	and protein; blood coagulation; Zsnk2; ds.	ı, therapy;
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ABX93674 standard; cDNA; 454 BP.
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                                                                             (first entry)
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                                                                                                                                                                                                                                                      Deinagkistrodon acutus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unstable angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
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                                                                             02-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                               thrombosis.
                                                   ABX93674;
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                                                                                                                                                                                                                                                                                 Key
              4BX93674
RESULT
                                                  The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
c aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
practical kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
proteins by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein, Zsnk2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                          which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
 /product= "Zsnk2 protein"
/note= "CDS does not include start codon"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 483 BP; 129 A; 112 C; 123 G; 119 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                               /*tag= c
/product= "Mature Zank2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 71-72; 79pp; English.
                                                                                                                                                                                                                  ; 2000US-225072P.
; 2000US-225087P.
; 2000US-225489P.
; 2000US-225490P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .47e-10
                                                                                                                                                                                         13-AUG-2001; 2001WO-US25310.
                                                                                                                                                                                                                                                                      2000US-356997P
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82.76%
75.86%
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/*tag= c
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                                                                                                                                                                                                                                                                                                                           Sheppard PO, Bishop PD;
                                                                   /*tag=
                                                     .. 59
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P-PSDB; AAE20178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    molecular biology
                                                                                                                                     WO200214364-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity
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14-AUG-2000;
15-AUG-2000;
15-AUG-2000;
20-DEC-2000;
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                                                        sig_peptide
                                                                                  mat_peptide
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/*tag= d
/note= "Unsequenced region could be 10-20 nucleotides in
                                                                   Antithrombosis; ss; PCR; beta chain; fibrin hydrolysis; blood clot; platelet aggregation; vaso-occulusive disorder; thromboembolic disorder; procardial infarction; restenosis; cancer; neurodegenerative disease; angiopathic thrombosis; cerebral thrombosis; thrombosis; oscillerans; ischaemic cerebral vascular disease; unstable angina; acute thrombosis; unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravencusly. Thrombosis enzyme was an atter the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.05 microlyfs and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis,
cDNA encoding Deinagkistrodon acutus antithrombosis enzyme beta chain.
                                                                                                                                                                                                                                                                                                                      peripheral arterial occulsion; stroke; atherosclerosis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (pos: 216 . . 218, aa: Xaa)
(pos: 219 . . 221, aa: Xaa)
(pos: 222 . . 224, aa: Xaa)
(pos: 225 . . 227, aa: Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme
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/note= "Mature beta chain"
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/product= "Antithrombosis
/product= "Antithrombosis
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/transl_except= (
/transl_except= (
/transl_except= (
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angiopathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thromboangiitis obliterans, pulmonary embolism, deep vain thrombosis, peripheral arterial occulsion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence repersents cDNA encoding the
                                                                                                                                                                                                                                                                                     1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agristrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snake venom blood anticoagulant halyxin B chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
                                                                                Deinagkistrodon acutus antithrombosis enzyme beta chain
                                                                                                          Sequence 454 BP; 114 A; 107 C; 114 G; 109 T; 10 other;
                                                                                                                                                     454
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Matches:
Conservative:
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                                                                                                                                                 2.67e-10
132.00
79.31%
72.41%
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encodes the B chain of he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOB-) BIOBUD CO LTD
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                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                  Alignment Scores:
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633 20

Length: Matches:

2,19e-09 127,00

Alignment Scores:

Pred. No.:

Score:

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1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                 Pigmy rattlesnake, venom gland protein; blood coagulation; therapy; platelet aggregation; gene; Zsnk3; ds.
  0010
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 Conservative:
Mismatches:
Indels:
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                                                                                                                                                     protein"
                                                                                                                                        29
                                                                                                                                     21 LysThrTrpThrAspAlaGluSerPhe
                                                           US-09-938-114-3 (1-29) x AAI71877 (1-633)
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                                                                                                                                                                                                                                                                                                                                                                                                                       'product= "Zsnk3
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14-AUG-2000; 2000US-225687P.
15-AUG-2000; 2000US-225499P.
15-AUG-2000; 2000US-325490P.
20-DEC-2000; 2000US-325690P.
                                                                                                                                                                                                                  DNA; 721
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160..546
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                        Sistrurus miliarius.
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P-PSDB; AAE20179.
                                                                                                                                                                                                                 AAD32055 standard;
Percent Similarity:
Best Local Similarity:
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                      Query Match:
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system. The polypeptides, which affect blood coagulation and
polynucleotide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jmy rattlesnake (Sistrurus miliarius) venom gland proteins, which blood coagulation and platelet aggregation system, useful in , and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pigmy rattlesnake venom gland protein Zsnk2, degenerate nucleic acid
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                                                                                                                                               Sequence 721 BP; 192 A; 167 C; 203 G; 159 T; 0 other;
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Mismatches:
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Matches:
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2000US-225489P.
2000US-225490P.
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74.71$
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                                                                                                                    protein, Zank3 gene
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Best Local Similarity:
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15-AUG-2000;
15-AUG-2000;
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platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory practical kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The polymolectide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal ages, mass spectrometry, circular dichroism to determine conformation or affinity chromatography columns to purify the protein, cloning or sequencing. The present sequence is Sistrurus miliarius venom gland
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                                                                                                                                                                                                                                                                                                                                                     1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korean adder; ss; salmorin protein B chain; snake venom;
fibrinogen clotting inhibition; thrombosis; prothrombin binding;
thrombin binding; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Korean adder snake venom salmorin B chain protein cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= c
note= "Mature Salmorin B chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Salmorin B chain protein"
                                                                                                                                                                                                                                  84 G; 70 T; 193 other;
                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7..444
/*tag= a
/product= "Salmorin B ch
7.75
/*tag= b
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                 degenerate nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AARACNIGGGAYGAYGCNGARWSNITY
                                                                                                                                                                                                                                                                                                                                                                                                            21 LysThrTrpThrAspAlaGluSerPhe
                                                                                                                                                                                                                                                                                                                               (1-453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agkistrodon halys brevicaudus.
                                                                                                                                                                                            74 A; 32 C;
                                                                                                                                                                                                                                                                                                                                 x AAD32054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL42016 standard; cDNA; 583
                                                                                                                                                                                                                                   2.17e-08
119.00
68.97%
62.07%
70.00%
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571..583
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                                                                                                                                                                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                             Sequence 453 BP;
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                                                                                                                                                                   protein Zšnk2,
                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL42016;
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                                                                                                                                                                                                                                                                                         Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
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us-09-938-114-3.rng

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The invention comprises the nucleotide and protein sequences of a salmorin protein derived from the venom of Korean adder. Salmorin protein is composed of an A chain and a B chain, and has inhibitory activity against fibrinogen clotting. The salmorin protein of the invention is useful for treating thrombosis, as it represses fibrinogen clotting potently by binding to prothrombin and thrombin so as to delay blood cogquiation. The present cDNA sequence encodes the Korean adder salmorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AspCysSerSerAspTrpSerSerTyrGluG1yHisCysTyrLysValPheLysGlnSer 20
                                                                                  New salmorin protein derived from venom of Korean adder Agkistrodon halys brevicaudus, useful for treating thrombosis by repressing fibrinogen clotting through repression of activation of prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   venom; halyxin; anticoagulant; thrombogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snake venom blood anticoagulant halyxin A chain coding sequence.
                                                                                                                                                                                                                                                                                    Sequence 583 BP; 151 A; 137 C; 150 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                              583
119
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 LysThrTrpThrAspAlaGluSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-938-114-3 (1-29) x AAL42016 (1-583)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koo
                                                                                                                                                Claim 1; Fig 1B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                           2.96e-08
119.00
68.97%
65.52%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                        Kim D, Koh Y;
(BIOB-) BIOBUD CO LID.
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                                                2002-241907/29
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                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snake; pit viper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agkistrodon halys
                                                             P-PSDB; AA014521
                                                                                                                                                                                                                                                              B chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-637330,
P-PSDB; AAM51543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; ds.
                                                                                                                         into thrombin
                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                        Chung K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI71876;
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1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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                                                The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence encodes the A chain of halyxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pigmy rattlesnake venom gland protein Zsnk3, degenerate nucleic acid.
Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rattlesnake; venom gland protein; blood coagulation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, affect blood coagulation and platelet aggregation system, useful itherapy and diagnostics, or as tools in the study of genetics or
                                                                                                                              BP; 166 A; 133 C; 163 G; 139 T; 0 other;
                                                                                                                                                                    601
19
2
8
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                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                          Claim 1; Page 9; 21pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-225072P.
; 2000US-225087P.
; 2000US-225489P.
; 2000US-225490P.
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119.00
72.41%
65.52%
70.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           platelet aggregation; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-269180/31
                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecular biology
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                                                                                                                                                                                          Percent Similarity:
                                                                                                                              Sequence 601
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15-AUG-2000;
                                                                                                                                                     Alignment Scores:
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-2002
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DB:
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70 GAYTGYCCNWSNGGNTGGWSNWSNTAYGAYCARCAYTGYTAYMGNGTNTTYAARCARYTN 129
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                            platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory practical kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The polymelectide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal agis, mass spectrometry, circular dichrism to determinal conformation or sequencing. The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
system. The polypeptides, which affect blood coagulation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding Deinagkistrodon acutus antithrombosis enzyme alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product= "Antithrombosis enzyme alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_except= (pos:244..246, aa:Lys)
/note= "No start codon given"
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118
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AARACNTGGGAYGAYGCNGARMGNTTY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein Zank3, degenerate nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LysThrTrpThrAspAlaGluSerPhe
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115.00
65.52%
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67.65%
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*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANGE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE 
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The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis was arsyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour collaborated administration at 0.05 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thrombosito, thrombosis, crebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thrombosis, atterial acculsion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents cDNA encoding the Deinagkistrodon acutus antithrombosis enzyme alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GluGlyHisCysTyrLysValPheLysGlnSerLysThrTrpThrAspAlaGluSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAATGCAGAGAGGCTTC
                                                                                         New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antithrombotic peptide; snake venom; platelet binding inhibition; von Willebrand factors; Crotalus horridus horridus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 544 BP; 158 A; 122 C; 143 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snake venom antithrombotic oligopeptide cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                           Example 3; Column 25-26; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-938-114-3 (1-29) x ABX93668 (1-544)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ89309 standard; cDNA; 690 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-JP01555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.05e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115.00
100.00%
100.00%
67.65%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crotalus horridus horridus
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(first entry)
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                                              WPI; 2003-352116/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                          P-PSDB; ABU08798
             Cheng X;
                                                                                                                                              unstable angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1994;
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               BX,
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93JP-0236975

22-SEP-1993;

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AAR71978 and AAR71979 are snake venom derived antithrombotic peptides, specifically from the snake venom oligopeptide AAR71981, encoded by AAQ89309. These peptides have the advantage of avoiding significant
                                                                                                                                                                                                                                                  thrombocytopenia when administered at the minimun dose, for in vivo inhibition of platelet von Willebrand factor binding. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Subunit peptide production; snake venom; rattlesnake; thrombolytic; von Willebrand's factor; blood platelet-inhibitory activity; ds.
                                                                                                                              Single-chain antithrombotic peptide - obtained by cleaving an oligopeptide from snake venom to break inter-chain disulphide bonds but preserve intra-chain disulphide bonds
                                                                                                                                                                                                                                                                                                    Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kayahara T,
                                                     Kito M, Kobayashi T,
Yoshimoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a snake venom derived protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ATGACCTGGGCCGATGCAGAGGTTC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                 Example 2; Pages 47-48; 84pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-938-114-3 (1-29) x AAQ89309 (1-690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
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111.00
72.41%
62.07%
65.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0096073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crotalus horridus horridus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO CO INC
                                                    Ishii K, K
Yamamoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukuchi N, Kageyama S,
                          (AJIN ) AJINOMOTO KK
                                                                                         WPI; 1995-139559/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-664985/64.
P-PSDB; AAY85628.
                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                                                                       P-PSDB; AAR71981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200059926-A1.
                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2000
                                                    Pukuchi N,
                                                                  ranaka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC61144;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                    Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC61144
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This invention relates to a method for the production of a subunit peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its subunit using a protein denaturing the subunit using a protein denaturing agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which reacts with a polyether lowup and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake women-originated dimer peptide with blood platelet-inhibitory activity on von Willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents marked at the protein used in an example illustrating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombolytic, glycoprotein Ib-binding protein; snake venom; rattlesnake; antithrombotic; glycoprotein Ib; long half life; low antigenicity; drug efficacy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Antithrombotic wild-type rattlesnake protein"
 Producing physiologically-active subunit peptides originating in polymer proteins by denaturation and specific separation, with lower antigenicity but improved solubility and stability, e.g. blood platelet-binding inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding the antithrombotic wild-type rattlesnake protein.
                                                                                                                                                                                                                                                                                                                       Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        690
118
3
8
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LysThrTrpThrAspAlaGluSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 ATGACCTGGCCGATGCAGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-690)
                                                                           Disclosure; Page 46; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
66..515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-938-114-3 (1-29) x AAC61144
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72.41%
62.07%
65.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                          method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK99834 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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Producing
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                         Nagano M;
                                                                                                                                                                                                                                                                                                                                                                                               690
118
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Matches:
Conservative:
Mismatches:
Indels:
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Ξ

Suzuki

Ishikawa K,

Futaki F,

Kito M, Kayahara T,

Fukuchi N,

(AJIN) AJINOMOTO CO

H;

04-OCT-2001; 2001EP-0123277 04-OCT-2000; 2000JP-0305279

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15-AUG-2000; 15-AUG-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-20000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-20000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-DEC-2000; 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                The invention relates to a glycoprotein Ib-binding protein, originating from snake venom, comprising specific mutations and antithrombotic activity. Glycoprotein Ib-binding protein is used in a drug having antithrombotic activity. Glycoprotein Ib-binding protein has a high binding activity to glycoprotein Ib, a long half life/drug efficacy retention in blood, and low antigenicity. This polymucleotide sequence represents DNA of the wild-type rattlesnake protein of the invention.
                                                                                                    Glycoprotein Ib-binding protein, useful for treating thrombosis, comprises specific mutations in protein originating from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pigmy rattlesnake, venom gland protein, blood coagulation, therapy; platelet aggregation; gene; Zsnk4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Zsnk4 protein"
/note= "CDS does not include start codon"
/partial
                                                                                                                                                                                                                                                                                                                                                         Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   690
118
3
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0
0
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mature Zsnk4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 ATGACCTGGGCCGATGCAGAGGTTC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-938-114-3 (1-29) x AAK99834 (1-690)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                             Example 1; Page 25; 49pp; English.
    Yamada N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2000; 2000US-225072P.
                                                                                                                                                                                                                                                                                                                                                                                                                 5.47e-07
111.00
72.41%
62.07%
65.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-2001; 2001WO-US25310
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      Shimba N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sistrurus miliarius.
                                        WPI; 2002-364482/40.
P-PSDB; AAO20974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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      Gondoh K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD32057;
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet venom gland proteins, which affect blood coagulation and platelet aggregation system. The polypeptides, which affect blood coagulation and platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful in therapy and diagnostics. The protein chemistry and antibody production and analysis. The protein chemistry and antibody production and analysis. The polymelectide or polypeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying proteins by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tass, mass spectromerry, dircular dichroism to determine conformation or sequencing. The present sequence is Sistrurus miliarius venom gland protein, Zsnk4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pigmy rattlesnake venom gland protein Zsnk4, degenerate nucleic acid.
                                                                                                                                                                                                                                                                                                                                     New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh
affect blood coagulation and platelet aggregation system, useful in
therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rattlesnake; venom gland protein; blood coagulation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 580 BP; 154 A; 133 C; 163 G; 130 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 75; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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2000US-225490P.
2000US-356997P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             platelet aggregation; ds
                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                       Sheppard PO, Bishop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sistrurus miliarius.
                                                                                                                                                                                                                                                 WPI; 2002-269180/31.
P-PSDB; AAE20180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200214364-A2.
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Agkistrodon halys brevicaudus

which

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)

venom gland proteins, which affect blood coagulation and platelet

dagregation system. The polypeptides, which affect blood coagulation and

platelet aggregation system, are useful in therapy and diagnostics. The

polypeptides are also useful as an educational tool in laboratory

proteins courses related to genetics and molecular biology,

protein chemistry and antibody production and analysis. The

polymucleotide or polypeptide can be used as standards or as unknowns

columnistry and purposes. The polypeptides are also useful in identifying

proteins by western bloctting, protein purification, determining the

weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal

tags, mass spectrometry, circular dichroism to determine conformation or

affinity chromatography columns to purify the protein, cloning or

sequencing. The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432
16
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein Zenk4, degenerate nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            x AAD32058 (1-432)
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 76; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL42015 standard; cDNA; 632 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 432 BP; 91 A; 34 C;
                                                                  2000US-225087P.
2000US-225489P.
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103.00
65.52%
55.17%
60.59%
                                                                                                    15-AUG-2000; 2000US-225490P.
20-DEC-2000; 2000US-356997P.
            13-AUG-2001; 2001WO-US25310
                                                  2000US-225072P
                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                             PD;
                                                                                                                                                                                             Bishop
                                                                                                                                                                                                                              WPI; 2002-269180/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-938-114-3 (1-29)
                                                                                                                                                                                                                                                                                                                   nolecular biology
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Best Local Similari
                                                                                                                                                                                           Sheppard PO,
                                                  14-AUG-2000;
                                                                  14-AUG-2000;
                                                                                   15-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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Korean adder; ss; salmorin protein A chain; snake venom; fibrinogen clotting inhibition; thrombosis; prothrombin binding; thrombin binding; blood coagulation. Korean adder snake venom salmorin A chain protein cDNA sequence. (first entry) 16-MAY-2002

AAL42015;

completed: December 8, 2003, 14:04:47

Search completed: December Job time: 100.594 secs

172 ACCTGGGAAGATGCAGAGGGTTC 195

22 ThrTrpThrAspAlaGluSerPhe

à

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The invention comprises the nucleotide and protein sequences of a salmorin protein derived from the venom of Korean adder. Salmorin protein is composed of an A chain and a B chain, and has inhibitory activity against fibrinogen clotting. The salmorin protein of the invention is useful for treating thrombosis, as it represses fibrinogen clotting potently by binding to prothrombin and thrombin so as to delay blood cognilation. The present cDNA sequence encodes the Korean adder salmorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CysSerSerAspIrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                               New salmorin protein derived from venom of Korean adder Agkistrodon halys brevicaudus, useful for treating thrombosis by repressing fibrinogen clotting through repression of activation of prothrombin
                                                                                                                         /*tag= c
/note= "Mature Salmorin A chain protein"
                                     34..498
/*tag= a
/product= "Salmorin A chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other;
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Conservative:
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                                                                                   /*tag= b
/note= "Signal peptide"
103..495
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                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A; 30pp; English.
                                                                                                                                                                                                                                                                                   27-JUL-2000; 2000KR-0043470.
                                                                                                                                                                                                                                                           26-JUL-2001; 2001WO-KR01277
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                                                                                                                                                                                                                                                                                                            (BIOB-) BIOBUD CO LTD
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-241907/29
                                                                                                                                                                                                                                                                                                                                   Chung K, Kim D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A chain protein
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257, App 1, Appli 5, Appli 5, Appli

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Sequence Sequence Sequence 1 Sequence

Sequence

Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence

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TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE VENOM OF AGKISTRODON ACUTUS
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09058740

Patent No. 6489451

GENERAL INFORMATION:
Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jing-Guo Ding, Fang Rong, Jing-Guo Ding, Fang Rong, Jing-Ran Chen
US-08-840-062-1
US-08-840-062-3
US-08-840-062-3
US-08-842-20-6034-1
US-07-778-156-4
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
Storage
                                                                                                                                                                                                                                                                                                                           US-08-543-246B-1
US-09-517-605-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <UNKNOWN> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Chen, Anthony C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
 RESULT 1
US-09-058-740-12
 Sequence 12, Appli
Sequence 1, Appli
Sequence 7, Appli
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Sequence 10, Appli
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Sequence 8, Appli
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                                                               2003, 13:49:04; Search time 22.8686 Seconds (without alignments) 559.725 Million cell.updates/sec
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     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-543-246B-14
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US-08-543-246B-8
US-09-996-243-318
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US-08-612-840A-7
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PCT-US95-03747-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5180808-1
                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
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Score

Result Š.

Database :

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                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-612-840A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                             US-09-058-740-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GATTGTCCCTCTGAGTGGTCCTCCTATGAGGGCATTGCTACAAGCCCTTCGATGAACCT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE VENOM OF AGKISTRODON ACUTUS
                                                                                                                                                                                                                                                                                 any base.
                                                                                                                                                                                                                                                                                                                                                                                              454
21
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Sequence 1, Application US/09058740
Patent No. 6489451
GENERAL INFORMATION:
APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and Hui-Ran Chen
                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                               LOCATION: 3...440
OTHER INFORMATION: "N" stands for "xa" stands for any amino acid SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-938-114-3 (1-29) x US-09-058-740-12 (1-454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/058,740 FILING DATE: 10-Apr-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                               Coding Sequence
               REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AAGACCTGGCCAGATGCAGAAATTC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
REGISTRATION NUMBER: 38,673
                                                                                                                                             LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          1.73e-11
132.00
79.31%
72.41%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                         US-09-058-740-12
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90
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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1 GAAGGGCATTGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAAGATGCTAGAAGGCTTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND TITLE OF INVENTION: METHOD OF PRODUCING THE SAME NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             N 2 0 0 0 0
4 0
4
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-938-114-3 (1-29) x US-09-058-740-1 (1-544)
                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
NAME: Chen, Anthony C.
REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFWARE: FastESQ Version 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/612,840A FILING DATE: 20-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
FILING DATE: 12-SEP-1993
NAME: No. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YANAMOTO, Hiroshi
APPLICANT: YANAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHI, Kolchi
APPLICANT: YOSHIMOTO, Ryota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/08612840A
; Patent No. 5856126
                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                             8.2e-09
115.00
100.00%
100.00%
67.65%
                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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us-09-938-114-3.rni

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5191 base pairs
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                                                                     TOPOLOGY:
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      LENGTH:
                                                                                                                                                                                                                                                                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GAATGTCCCTCCGGTTGGTCTTCCTATGATGGTATTGCTACAAGCCCTTCAAACAAGAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES:
ADORESPENDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CITY: Washington
STATE: D.C.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 ATGACCTGGGCCGATGCAGAGAGGTTC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELEPHONE: 202-628-5197
                                                                                                                                                                          ORGANISM: Crotalus horridus horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08340428B
Patent No. 5648465
LENGTH: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                              4.44e-08
111.00
72.41%
62.07%
65.29%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                  JS-08-612-840A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-340-428B-1
                                                                                                                                                                                            STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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3161 IGGBACCGIGGCACAAATICCAGGGCCACIGCIACCGCIACTIIGCICAICGGCGG 3220
                                                                                                                                                                                                                                                                                                                                                                                                                               2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, UWe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
CORRESPONDENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07306
FILING DATE: 03-AUG-1993
APPLICATION NUMBER: US 07/922,911
FILING DATE: 03-AUG-1992
ATTORNEY AGENT INFORMATION:
NAME: Townsend, Guy K.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: Margolis=1A PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                US-09-938-114-3 (i-29) x US-08-340-428B-1 (1-5191)
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                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9307306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3221 GCCTGGGAGGACGCAGAG 3238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ThrTrpThrAspAlaGlu 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 84.00
57.69%
42.31%
49.41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5191 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202-737-3528
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                 77..3847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 419 cc...
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
7TP: 20004
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LOCATION: 77..3847
                                                            MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                      ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77...
US-08-340-428B-1
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2176 TGCAGCCCCGGTTGGGACGCCTTCCAGGGTGCCTGCTACAAGCACTTTTCTGCCCCGAAGG 2235
                                                                      2236 AGCTGGGAGGAGGCGGAGAAC 2256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
                                        22 ThrTrpThrAspAlaGluSer 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6870 ACATGGGATGCAGCTGAA 6887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ThrTrpThrAspAlaGlu 27
                                                                                                                                                                                                                                                                                                                                                                                                                            75.00
53.85%
42.31%
44.12%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                    LENGTH: 8224
                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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US-08-543-246B-10
                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                  SEQ ID NO:1
                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                  5180808-1
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                                                                                                                                                                                                                                             3161 TGCGACCGTGGCTGCACAAATTCCACGCCACTGCTACCTTTGCTCATCGGCGG 3220
                                                                                                                                                                                                                        CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
INUMBER OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                    US-09-938-114-3 (1-29) x PCT-US93-07306-1 (1-5191)
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                                                         Length:
Matches:
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Matches:
                                                                                                                                  Indels:
                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION UNDRER: 37,643
REFERENCE/DOCKET NUMBER: FP-L.
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 535-9001
TELEPAK: (619) 535-9001
TELEPAK: (619) 535-949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                3221 GCCTGGGAGGACGCAGAG 3238
                                                                                                                                                                                                                                                                                             22 ThrirpThraspAlaGlu 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                        84.00
57.69%
42.31%
49.41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.00
66.67%
40.74%
46.47%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112..2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                             Best Local Similarity:
                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
PCT-US95-03747-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
PCT-US93-07306-1
                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-03747-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                Query Match
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6810 IGTGACTATGGCTGGCACAAATTCCAAGGGCAGTGCTACAAATACTTTGCCCATCGACGC 6869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells
NOMBER OF SEQUENCES: 24
NOMBER OF SEQUENCES: ADDRESSE: ADDRESSEE: Michael W. Glynn
ADDRESSEE: Mo. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
APPLICAMY: RUOSLAHTI, ERKKI I.
TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/07/441,179
PILING DATE: 27-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FLING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FLING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/122,514
FLING DATE: 24-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-114-3 (1-29) x 5180808-1 (1-8224)
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US-08-543-246B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-055-095-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPhcLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA and amino acid sequence specific for natural killer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Kassenoff, Melvyn M.

REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
TELEPAX: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 base pairs
TENGTH: 402 base pairs
TENGTH: acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
TITLE OF INVENTION: DNA and amino acid sequentified of INVENTION: natural killer cells
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: Michael W. Glynn
ADDRESSEE: Mo. 6262244artis Corporation
STREET: 564 Morris Avenue
COTY: Summit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-938-114-3 (1-29) x US-08-543-246B-10 (1-402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AACTGGTATGAGAGCCAGGCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ThrTrpThrAspAlaGluSer 28
                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       73.00
66.67%
33.33%
42.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-543-246B-14
                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
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Patent No. 5945308
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
OWNERSPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASTSRQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
          118-7704/PCT/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-114-3 (1-29) x US-08-543-246B-14 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 35,749
REFERENCE/DOCKET NUMBER: PF-0500 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 AACTGGTATGAGAGCCAGGCT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ThrTrpThrAspAlaGluSer 28
REFERENCE/DOCKET NUMBER: 118-
TELEPHONE: 908-522-6927
TELEPHONE: 908-522-6927
TELEPAX: 908-522-6927
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTER.STICS:
LENGTH: 648 base pairs
TYPE: nucleic acid
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      73.00
66.67%
33.33%
42.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                              HYPOTHETICAL: NAME ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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us-09-938-114-3.rni

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NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-996-243-318
                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                        US-08-543-246B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                             446 TGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAA 505
                                                                                                                                                                                                                                                                                                                                                                        CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPP PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
FILING DATE: 28-MAR-1991
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SED-1993
ATTORNEY AGENT THORMATION:
NAME: KASSENOFF, MALVAN M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET UNMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
                                                                                                                                                                                                                                                                                                                                  JS-09-938-114-3 (1-29) x US-09-055-095-2 (1-1740)
                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 AGTIGGGAGGACTGTAATATITC 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                            73.00
60.71$
35.71$
42.94$
                                                                                                                                                                                        0.0803
TYPE: nucleic acid
STRANDEDNESS: single-
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                 LIBRARY: LUNGNOT09;
CLONE: 1355922
US-09-055-095-2
                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                     Alignment Scores:
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STATE: N.
COUNTRY:
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2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                      US-09-938-114-3 (1-29) x US-08-543-246B-8 (1-1755)
                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693 AACTGGTATGAGAGCCAGGCT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 318, Application US/09996243
Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ThrTrpThrAspAlaGluSer 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grimaldi,J.Christopher
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  errara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerber, Hanspeter
                                                                                                                                                                                                                          0.0811
73.00
66.67%
33.33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ashkenazi, Avi J.
                                                                                                                                mat_peptide
339..986
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Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eaton, Dan L.
                                                                                               339..986
                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-06-17
PRIOR PELICATION NUMBER: 60/08959
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089601
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
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PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06

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2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08840062
Fatent No. 611797
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: LASKY, LAURENCE A.
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 AGTTGGGAGGÁCTGTAAATATTTC 635
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                          PRIOR FILLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091632
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091948
PRIOR APPLICATION NUMBER: 60/091949
PRIOR APPLICATION NUMBER: 60/091942
PRIOR APPLICATION NUMBER: 60/092182
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4588 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.086
73.00
60.71%
35.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
4588
7
11
9
0
 Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              US-09-938-114-3 (1-29) x US-08-840-062-1 (1-4588)
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                                                                  Indels:
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ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1019R1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 187525-3316
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TILLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                   1302 CGCAGCTGGCAGAGTCCAAG 1322
                                                                                                                                                                                                              21 LysThrTrpThrAspAlaGlu 27
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; Patent No. 6117977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4771 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
 0.264
73.00
66.67%
25.93%
42.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.277
73.00
66.67%
25.93%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-114-3 (1-29)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                Query Match:
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by similarity with known sequence or to
an established consensus
                                                                                                     Sequence 1, Application US/08220603A
Patent No. 5612190
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A Bovine Group I Phospholipase A2 Receptor NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: N
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10020
COMPUTER 10020
COMPUTER 10020
COMPUTER 10020
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS ver. 2.11
SOFTWARE: Word Perfect (ASCII file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,603A
FILING DATE: 30-MAR-1994
FILING DATE: 30-MAR-1993
APPLICATION NUMBER: JP 5-72323
FILING DATE: 30-MARCh-1993
APPLICATION NUMBER: JP 6-40177
FILING DATE: 10-MARCh-1994
FILING DATE: 10-MARCh-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4978
TVOR: nucleic acid
1213 CGCAGCTGGCAGGAGTCCAAG 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY: CDS

LOCATION: 280 to 4668

LOCATION: 120 to 4668

LOCATION: 120 to 4668

LOCATION: 120 to 4668

LOCATION: 200 to 4668

LOCATION: 200 to 4668

LOCATION: 200 to 4668

LOCATION: 200 to 4668
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Pred. No.:
                                                                                            US-08-220-603A-1
                                                                      RESULT 15
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||| ||| TGTGAGCCTGGCTGGAATCCCCACAAATGCTATAAACTGCAGAAAAAAAG 1470 2 CysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-938-114-3 (1-29) x US-08-220-603A-1 (1-4978) Gaps: 0.414 72.00 64.00% 40.00% Percent Similarity: Best Local Similarity: Query Match:

Score:

1471 ACCTGGAATGAGGCT 1485

22 ThrTrpThrAspAla 26

g ઠે Search completed: December 8, 2003, 17:27:03 Job time : 25.8686 secs

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Page

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Sequence 10, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 5299, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50, Applisequence 5, Applisequence 5, Applisequence 73, Applisequence 73, Applisequence 87, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, Applisequence 51, A
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Sequence 7, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
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Sequence 19, Appl
Sequence 1, Appli
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Sequence
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APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
TITLE REPERRINCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                    US-09-929-230-1; Sequence 1, Application US/09929230; Patent No. US20020161203A1
; GENERAL INFORMATION:
 ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (3) ... (455)
NAME/KEY: misc. Eacture
LOCATION: (0) ... (0)
OTHER INFORMATION: Zsnk2
                                                                                                                                                                                                                                                                                                                                                                           512
6310
6230
629
629
2652
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2652
31153
31153
3153
634
634
634
LENGTH: 483
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103
97
97
                                                                                                                                                                                                                                                                                                   TYPE: DNA
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-MODEL=frame+ p2n.model.-DEV=xlh
-Q=/cgn2 1/USPTO_spool/USO9938114/runat_08122003_091002_22963/app_query.fasta_1.725
-Q=/cgn2 1/USPTO_spool/USO9938114/runat_08122003_091002_22963/app_query.fasta_1.725
-DB=Published Applications NA -CFMT=fastap -SUFFIX=npb -MINMATCH=0.1
-LCOPCLL=0 -LCOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=cto -NORM=ext -HRAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09938114 @CGN 1 1 504 @runat_08122003_091002_22963
-NCPUG -ICPUG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -NORM-DSPENCE=10 -XGAPEXT=0.5
-FGAROP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                            (without alignments)
835.675 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           8, 2003, 16:08:50 ; Search time 115.337 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*

1. \cgn2_6/ptodata/2/pubpia/USO7_pubCOMB.seq:*
2. \cgn2_6/ptodata/2/pubpia/PCT_MBW_PUB.seq:*
3. \cgn2_6/ptodata/2/pubpna/USO6_NBW_PUB.seq:*
4. \cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5. \cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6. \cgn2_6/ptodata/2/pubpna/USO8_NBW_PUB.seq:*
7. \cgn2_6/ptodata/2/pubpna/USO8_NBW_PUB.seq:*
8. \cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9. \cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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17. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
17. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
18. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
19. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
11. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
18. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
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18. \cgn2_6/ptodata/2/pubpna/USO0_NBW_PUB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                  using frame_plus_p2n model
                                                                                                                                                                                                                 170
1 DCSSDWSSYEGHCXKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                         2201672 segs, 1661799599 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

ijΩ

Query Match Length DB

Score

Result No.

0.5

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

US-09-938-114-3

Title: Perfect score:

Sequence:

nucleic search, December

OM protein -

Run on:

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Query Match:
DB:
                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                            1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                US-10-226-420-1

| Sequence 1, Application US/10226420
| Publication No. US20030157686A1
| GENERAL INFORMATION:
| APPLICANT: Sheppard, Paul O. | APPLICANT: Bishop, Paul D. | TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS FILE REPERENCE: 00-72
| CURRENT APPLICATION NUMBER: US/10/226,420
| CURRENT APPLICATION NUMBER: US/10/226,420
| CURRENT FILING DATE: 2002-08-21
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: FastSEQ for Windows Version 4.0
| TENTION OF 1
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APPLICANT: Shisppard, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
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                                                                                                                             US-09-938-114-3 (1-29) x US-09-929-230-1 (1-483)
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                                                                                             Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.24e-12
134.00
82.76%
75.86%
78.82%
                  1.24e - 12
                               134.00
82.76%
75.86%
78.82%
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) LOCATION: (0) ... (0)

) OTHER INFORMATION: Zsnk2

US-10-226-420-1
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NAME/KEY: CDS
LOCATION: (3)...(455)
FEATURE:
                                    Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Alignment Scores:
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US-09-929-230-4
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DB:
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Sequence 4, Application US/10226420; Publication No. US20030157686A1; Publication No. US20030157686A1; GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Blishop, Paul D.

TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS; FILE REPERENCE: 00-72; CURRENT FILING DATE: 2002-08-21; NUMBER OF SEQ ID NOS: 14; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 4; LENGTH: 721
                                                                                                                                                                                                                                        721
21
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6
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Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                 Gaps:
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 721
                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                      TYPE: DNA
CRGANISM: Sistrurus miliarius
FRATURE:
NAME/KRY: CDS
LOCATION: (91)...(546)
NAME/KRY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: ZSDK3
US-09-929-230-4
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127.00
79.31%
72.41%
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127.00
79.31%
72.41%
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| LOCATION: (0)...(0)

| OTHER INFORMATION: Zsnk3

US-10-226-420-4
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LOCATION: (91)...(546)
FEATURE:
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERTURE:
OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
NAME/KEX: misc feature
LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57, LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162, LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162, LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324, OTHER INFORMATION: n = A,T,C or G
NAME/KEX: misc feature
LOCATION: 330, 334, 339, 348, 351, 357, 360, 366, 372, 390, 393, OTHER INFORMATION: n = A,T,C or G
OTHER INFORMATION: n = A,T,C or G
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                              Sequence 3, Application US/09929230
FREENT NO. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Bishop, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Fublication No. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: RATLESNAKE VENOM GLAND PRC:
FILE REPERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-114-3 (1-29) x US-09-929-230-3 (1-453)
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21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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119.00
68.97%
62.07%
70.00%
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Best Local Similarity:
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LENGTH: 453
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1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                          NAME/KEY: misc feature
LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
LOCATION: 168, 171, 177, 180, 189, 192, 204, 210, 213, 219, 222,
LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393, LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
OTHER INFORMATION: n = A,T,C or G
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Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
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Patent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROFILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                         US-09-938-114-3 (1-29) x US-10-226-420-3 (1-453)
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119.00
68.97%
62.07%
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ORGANISM: Artificial Sequence
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115.00
65.52%
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CURRENT FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: JP 2000-305279
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FUTAKI, FUMIE
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SUZUKI, EIICHIRO
GONDOH, KEIKO
SHIMBA, NOBUHISA
                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
               NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                           CITY: Los Angeles
                                                                                                                                                  STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                               70 GAYTGYCCNWSNGGNTGGWSNWSNTAYGAYCARCAYTGYTAYMGNGTNTTYAARCARYTN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                          1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAMB/KEY: misc_feature
LOCATION: 282, 281, 309, 312, 321, 327, 330, 333, 336, 339, 360,
LOCATION: 366, 372, 378, 381, 384, 393, 396, 414, 429, 441, 447, 456
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 6, 9, 21, 24, 30, 33, 36, 39, 42, 48, 51, 54, 57, 60, 63,
LOCATION: 66, 69, 78, 81, 84, 90, 93, 114, 117, 129, 135, 147, 153,
LOCATION: 162, 171, 177, 180, 186, 189, 192, 201, 204, 213, 216, 222,
LOCATION: 225, 231, 234, 237, 246, 249, 252, 255, 261, 276, 279
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09938114
Publication No. US20030022350A1
GENERAL INFORMATION:
APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng,
Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
Jin-Guo Ding, Fang Rong, Yan Liu and
Hui-Ran Chen
TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                               Sequence 6. Application US/10226420
Publication No. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TILLE OF INVENTION: RATTLESNAKE VENOM GLAND IF FILE REPERRANCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
US-09-938-114-3 (1-29) x US-09-929-230-6 (1-456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AARACNTGGGAYGAYGCNGARMGNTTY 156
                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                           21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.53e-09
115.00
65.52%
62.07%
67.65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                             RESULT 8
US-10-226-420-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 456
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US-09-938-114-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
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DB:
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APPLICANT: YAMADA, NAOYUKI
TITLE OF INVENTION: PROPEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING
FILE REPREBENCE: 214760USO
CURRENT APPLICATION NUMBER: US/09/969,763
CURRENT FILING DATE: 2000-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAAGGGCAITGCTACAAGGTCTTCAAACAATCTAAGACCTGGACAGATGCAGAAGAGCTTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 GluGlyHisCysTyrLysValPheLysGlnSerLysThrTrpThrAspAlaGluSerPhe 29
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VENOM OF AGKISTRODON ACUTUS
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Matches:
Conservative:
Mismatches:
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,114
FILING DATE: 23-Aug-2001
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION NUMBER: 09/058,740
FILING DATE: «UNKnown»
APPLICATION NUMBER: «OP/058,740
FILING DATE: «UNKnown»
                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Chen, Anthony C.
REGISTRATION NUMBER: 38,673
REGISTRATION NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 949-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
TELEFAX: 67-3510
TELEFAX: 67-3510
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TELEFAX: 67-3510
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09969763; Publication No. US20020198363A1; GENERAL INFORMATION:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                    36 GATTGTCCCTCTGATTGGTATGCCTATGATCAGTATTGCTACAGGGTCATCAAACAACTC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09929230
Patent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 580
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118
3
8
0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   201 ATGACCTGGGCCGATGCAGAGGTTC 227
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PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                              1.18e-08
111.00
72.41%
62.07%
65.29%
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110.00
75.86%
58.62%
64.71%
                                                                            TYPE: DNA ORGANISM: Crotalus harridus
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LOCATION: (3) ... (434)

NAME/KEY: misc feature

LOCATION: (0) ... (0)

OTHER INFORMATION: Zsnk4
US-09-929-230-7
                                                                                                                     NAME/KEY: CDS
; LOCATION: (66)..(512)
; OTHER INFORMATION:
US-09-969-763-2
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Best Local Similarity:
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Query Match:
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Pred. No.:
                                                            LENGTH: 690
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                                                                                                          FEATURE
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Sequence A Application UB/1026420
| Particular Application UB/1026420
| Particular Sequence A Application UB/1026641
| Particular Sequence A Sequence A Sequence A Sequence A Particular Sequence A Particular Sequence A Particular Sequence A Particular Sequence A Particular Sequence A Particular Sequence A Particular Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Sequence A Se
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Search completed: December 8, 2003, 19:36:05 Job time: 116.337 secs
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DB:
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                                                                                                                                                                                                                                                                        34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGYTAYMGNGTNATHAARCARYTN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature

LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 111,

LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180,

LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276,

LOCATION: 285, 291, 297, 300, 315, 327, 330, 345, 348, 360

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-226-420-9
; Sequence 9, Application US/10226420
; Sequence 9, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432
16
3
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116
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: LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426

: COCATION: n = A,T,C or G

US-10-226-420-9
                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                94 MGNACNTGGGAYGAYGCNGARMGNTTY 120
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                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                              21 LysThrTrpThrAspAlaGluSerPhe 29
; OTHER INFORMATION: n = A,T,C or GUS-09-929-230-9
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103.00
65.52%
55.17%
60.59%
                                                                             1.34e-07
103.00
65.52%
55.17%
                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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94 MGNACNTGGGAYGAYGCNGARMGNTTY 120

RESULT 15

21 LysThrTrpThrAspAlaGluSerPhe 29

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163 AATTGTCCTCTGGTTGGTTGGCTACGATCAGTATTGCTACAGGGTCATCAAACGACTC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
Sequence 10, Application US/09929230
Fatent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REPERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT PILING DATE: 2001-08-13
NUMBER: OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0.
ILENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                              725
15
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 AAGACCTGGGACGATGCAGAGCGGTTC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 LysThrTrpThrAspAlaGluSerPhe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.52e-06
97.00
72.41%
51.72%
                                                                                                                                                                                                                                                                       ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (88) ...(561)
NAME/KEY: misc.feature
LOCATION: (0) ...(0)
OTHER INFORMATION: Zsnk5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-929-230-10
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

sw model - protein search, using OM protein

December Run on:

8, 2003, 09:49:54; Search time 5.8 Seconds (without alignments)
480.843 Million cell updates/sec

170 1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF US-09-938-114-3 Title: Perfect score:

Sequence:

29

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

A47267 botrocetin alpha of alboagreghn-B alpegoreghn-B alpegoreghn-B alpegoreghn-B alpegorethn batha a53088 A53089 coagulation factor IX/factor X absolution factor alboaggreghn-B bet adopted and agretin alpha cha agretin alpha cha agretin alpha cha agretin alpha cha agretin alpha cha b53089 A3869 factor IX/factor X added B5308 factor IX/factor X added A3869 aggrecan precursor agrecan precursor aggrecan precursor aggrecan precursor aggrecan - bovine aggrecan - bovine aggrecan - bovine aggrecan - bovine A28452 A28452 aggrecan - bovine aggrecan core aggrecan precursor aggrecan aggrecan precursor aggrecan precursor aggrecan precursor aggrecan precursor aggrecan aggreca
24127 66006 66006 6829 6829 77027 77
555000 442972 5556829 5556829 553088 553088 553088 339808 339808 339808 339808
42972 A56829 PC7027 PC7027 A38609 A38609 A39086 A39808 A39808 A39808 A39808 A39808 A39808 A39808
PC4421 B53088 150421 150421 A39086 A39086 A39486 A39452 A58452
B53088 A38609 150421 A39086 A39808 T42630 A5182 A55182
A38609 150421 A39808 A39808 A28452 A55182
150421 A39086 A39808 A42630 A29452 A55182

neurocan - mouse	phospholipase A2 r	prevican precursor	pancreatic thread	brevican precursor	brevican precursor	NKR-P1 protein hom	brevican - human (chondroitin sulfat	echinoidin - sea u	versican - piq-tai	secretory phosphol	secretory phosphol	versican precursor	versican precursor	
S52781	A49707	S57653	A37194	849126	A54423	B46467	T46256	A47171	A26697	843922	B56395	A56395	T14274	A55535	A60979
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1268	1458	883	175	883	912	223	330	3562	147	862	1326	1465	1643	2397	2409
49.4	48.8	48.2	47.1	47.1	46.5	44.7	44.7	44.7	44.1	44.1	44.1	44.1	44.1	44.1	44.1
84	83	82	80	80	79	16	97	16	75	75	75	75	75	75	75
20	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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agkisacutacin alpha chain precursor - sharp-nosed viper
NyAlternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Decies: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: UC7134; PC7037
C;Accession: UC7134; PC7037
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 533-535, 1999
A;Title: Purification, characterization, and conva cloning of a new fibrinogenlytic venom
A;Reference number: UC7134; MUID:20025379; PMID:10558903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disnlifide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: venom gland
                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 1-152 <CHE>
A,Cross-references: GB:AF176420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 27; Conserv
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Coagulation factor IX/factor X-binding protein chain A precursor - habu C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Daces: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C;Acces: 10-Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem: Biochys. Res. Commun. 220, 382-387, 1996
A;Fitle: CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from si A;Reference number: JC4690; MUID:96184662; PMID:8645314

A;Accession: JC4691 A;Molecule type: mm1A A;Residues: 1-146 ckAll>
A;Coss-references: DDBJ:DB3332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642 A; Experimental source: venom

R;Atoda, H.; Hyuga, M.; Morita, T.

Biol. Chem. 266, 14803-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolate otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin B.

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R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oze
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: JC4329

A,Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A,Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavor A,Reference number: JC4329; MUID:96318509; PMID:8749314
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C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7105
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet.
A;Reference number: PC7027; MUID:99443731; PMID:10512747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 13-Mar-1998
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C;Comment: This protein binds calcium.
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; calcium binding; venom
F;2-127/Domain: C-type lectin homology <LCH>
F;2-13,30-127,102-119/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 128; DB 2; Length 129;
Pred. No. 4.1e-09;
0; Mismatches 7; Indels
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C, Superfamily: tetranectin; C-type lectin homology
C, Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coagulation factor IX-binding protein A chain - habu C;Species: Trimeresurus flavoviridis (habu)
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 129; DB 2;
Pred. No. 3e-09;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CLPDWSSYKGHCYKVEKVEKTWADAEKF 31
                                                                                                                                                                                                                                                                                                                           C;Keywords: venom F;4-121/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF
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   source: snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.9%;
Best Local Similarity 75.0%;
Matches 21; Conservative 1
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Best Local Similarity 75.9%;
Matches 22; Conservative
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Best Local Similarity 69.0
Matches 20; Conservative
                                                                                                                   A; Reference number: JC5916
                                                                                                                                                                               A; Molecule type: protein
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                  A;Accession: B39332
A;Molecule type: protein
A;Rodaule type: protein
A;Rodaule type: Drotein
A;Rodaule type: Drotein
B;Atodaule type: Drotein
T: Shikkawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
J. Biochem. 118, 965-973, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav
A;Reference number: JC4329; MUID:96318509; PMID:8749314
A;Accession: JC4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agkisacutacin beta chain precursor - sharp-nosed viper
N,Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
A;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
A;Tible: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom A;Reference number: JC7134; MUID:20025379; PMID:10558903
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Ditiscetin beta chain - puff adder

C;Species Itis arietans (puff adder)

C;Species Itis arietans (puff adder)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999

C;Accession: JCSOS9; JCS917

C;Accession: JCSOS9; JCS917

C;Accession: JCSOS9; JCS917

A;Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor A;Reference number: JCSOS9

A;Reference number: JCSOS9

A;Recious type: protein

A;Residues: 1-125 <AAT>
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F)24-1446/Product: factor IX/X binding protein chain B #status predicted <MAT>
F)25-142/Domain: C-type lectin homology <LCH>
F)25-36,53-142,119-134/Disulfide bonds: #status predicted
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A,Molecule type: protein
A,Residues: 24-50,59-83;102-107;112-114 <CH2>
C,Superfamily: tetranectin; C-type lectin homology
C,Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133; DB 2; Length 14
Pred. No. 1.1e-09;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Mesidues: 24-146 AAT2-
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; lectin; venom
number: A39332; MUID:91332000; PMID:1831197
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A;Cross-references: GB:AF176421
A;Experimental source: venom gland
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1 Similarity 72.4%;
21; Conservative
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Conservative
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Best Local Similarity
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52

A; Experimental source: venom

A; Molecule type: mRNA A; Accession: JC4690

A; Molecule type: protein A, Residues: 24-152 <ATO>

A;Status: preliminary

A;Accession: A39332

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R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modul.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIP:124086)
R;Pujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug:
Bochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally dis
A;Reference number: A37958; MUID:91129280; PMID:1993206
                               C;Accession: JC5058; JC5916

R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz. Submitted to JIPID, January 1997

A;Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dotrocetin beta chain - jararaca
NyAlternate names: two chain botrocetin beta chain
NyAlternate names: two chain botrocetin beta chain
CiSpecies: Bothrops jararaca (jararaca)
CiSpecies: Bothrops jararaca (jararaca)
CiSpecies: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
CiAccession: B47267; C37958
Ridsami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator jareference number: A47267; MUID:93157385; PMID:8430107
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0
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C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: venom
C,Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
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C;Keywords: hemagglutinin; heterodimer; venom
F;2-121/Domain: C-type lectin homology <LCAC
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental
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A,Residues: 1-40 <FUJ>
C,Complex: heterodimer of alpha (see PIR:A47267) and beta chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 119; DB 2; Length 125;
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2; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 1-131 <MAT>
A,Experimental source: snake venom
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Matches 19; Conservative
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A;Residues: 1-125 <USA>
A;Experimental source: venom
                                                                                                                                                                                     A; Reference number: JC5058
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                                                                                                                                                                                                                                 A; Contents: snake venom
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J. Biol. Chem. 266, 14903-14911, 1991
A;Title The primary structure of coagulation factor IX/factor X-binding protein isolate otein, terranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
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*Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
R;Kawasaki, T: Taniuchi, Y; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai
Biochem. J. 308, 947-953, 1995
A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib a
A;Reference number: S56006; MUID:97104297; PMID:8948455
                                                                                                                                                                                                     Coagulation factor IX/factor X-binding protein chain A precursor - habu Cispecies: Trimeresurus flavoviridis (habu)
Cjate: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
CjAccession: JC4690, A39332
R;Matsuzaki, R; Yoshiara, E; Yamada, M; Shima, K; Atoda, H; Morita, T.
Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: CDNA cloning of IX/A-BP, a heterogeneous two-chain anticoagulant protein from A;Reference number: JC4690; MUID:96184662; PMID:8645314
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(Keywords: anticoagulant; blood coagulation; glycoprotein; hemolymph; lectin
(1.23) Domain: signal sequence #status predicted <51G>
(24-152/Product: factor IXX binding protein chain A #status predicted <MAT>
(25-150/Domain: C-type lectin homology <LCH>
(1.25-150,125-142/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Residuce: 1-152 - MAT1>
A,Cross_references: DDBJ:D8331; NID:g1402639; PIDN:BAA11887.1; PID:g1402640
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Query Match 72.4%; Score 123; DB 2 Best Local Similarity 74.1%; Pred. No. 2e-08; Matches 20; Conservative 2; Mismatches

1 DCSSDWSSYEGHCYKVFKOSKTWTDAE 27 DCLSGWSSYEGHCYKAFEKYKTWEDAE 50

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RESULT 8

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bitiscetin alpha chain - puff adder
N/Alternate names: von Willebrand factor modulator protein
C/Species: Bitis arietans (puff adder)

1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29

Conservative

Local Similarity nes 19; Conserv

Best Loca Matches

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Query Match

A; Molecule type: protein A; Residues: 1-40 < KAW>

11

RESULT

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C;Comment: This protein inhibits agglutination of fixed platelets induced by several plat libbrand factor and albosgregins. C;Superfamily: tetranectin; C-type lectin homology C;Superfamily: tetranectin; dimer C;Keywords: anticoagulant; dimer
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R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai, Biochem. J. 308, 947-953, 1995
A;Title: Tokaracctin, a new platelet antagonist that binds to platelet glycoprotein Ib ar A;Reference number: S56006; MUID:97104297; PMID:8948455
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R,Sekiya, F.; Atoda, H.; Morita, T.
Biochemistry 32, 6892-6897, 1993
A,Title: Isolation and characterization of an anticoagulant protein homologous to botroce A,Reference number: A53088; MUID:93326575; PMID:8334120
                                             A;Title: Isolation, characterization and amino acid sequence of echicetin beta subunit, A;Reference number: JC2415; MUID:95091801, PMID:7999097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
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C.Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
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N;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
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C,Superfamily: tetranectin; C-type lectin homology
                 Biochem. Biophys. Res. Commun. 205, 68-72, 1994
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Best Local Similarity 62.1%;
Matches 18; Conservative
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Conservative
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A; Molecule type: protein
A; Residues: 1-123 < PEN>
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Best Local Similarity
Matches 19; Conserv
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Matches 18; Conserv
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A:Rexperimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBIP:124085)
A:Note: sequence extracted from NCBI backbone (NCBIP:124085)
B:Note: sequence extracted from NCBI backbone (NCBIP:124085)
B:Stylimus, Y:; Titani, Y: Josami, Y:; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug Biochemistry 30, 1957-1964, 1991
A:Title: Isolation and chemical characterization of two structurally and functionally di A:Reference number: A37958; MUD:91129280; PMID:1993206
A:Reference number: A37958; MUD:91129280; PMID:1993206
A:Residues: 1-40 cFUJ
C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Complex: hemagglutinin; heterodimer; venom
C;CyEywords: hemagglutinin; heterodimer; venom
C;CyEywords: hemagglutinin; heterodimer; wenom
C;CyEywords: hemagglutinin; heterodimer; wenom
F;2-128/Domain: C-type lectin homology cLCH>
F;2-13,30-128,103-120/Disulfide bonds: #status experimental
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C;Species: Trimeresurus albolabris (green pit viper)
C;Species: Trimeresurus albolabris (green pit viper)
C;Species: Trimeresurus albolabris (green pit viper)
C;Species: Trimeresurus albolabris (green pit viper)
C;Accession: B56829
R;Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.;
Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993
A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous A;Reference number: A56829; MUID:93221514; PMID:8466514
A;Accession: B56829
A;Accession: B56829
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A;Accession: C;Accession: C-type: Drotein
A;Residues: 1-40 cYOS-
A;Accession: C-type lectin homology
C;Acywords: disulfide bond; heterodimer
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A47267

Dotrocetin alpha chain - jararaca

Dotrocetin alpha chain

N;Alternate names: two chain botrocetin alpha chain

C;Species: Bothrops jararaca (jararaca)

C;Decies: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998

R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993

A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator ]

A;Reference number: A47267; MUID:93157385; PMID:8430107
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C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 15-Oct-1996
C;Accession: JC2415
R;Peng, M.; Holt, J.C.; Niewiarowski, S.
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67.6%; Score 115; DB 2; Length 40
67.6%; Pred. No. 6.4e-08;
7. 1%; Pred. no. 6.4e-08; Indels
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Matches 18; Conservative
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Query Match

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